review

S14 41 RD (unique items)
? t s14/7/all

14/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09968411 BIOSIS NO.: 199598423329
Genetic polymorphism of cereals revealed by **PCR** with random **primers**.
AUTHOR: Sivolap Yu M; Kalendar' P N; Chebotar S B
AUTHOR ADDRESS: Plant Breed. Genet. Inst., Ukr. Acad. Agrar. Sci., Odessa **Ukraine
JOURNAL: Tsitologiya i Genetika 28 (6):p54-61 1994
ISSN: 0564-3783
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Russian; Non-English
SUMMARY LANGUAGE: Russian; Ukrainian; English

ABSTRACT: **Polymerase chain** reaction of DNA amplification with the use of random **primers** is a new approach in investigations of genome specificity. Nucleotide sequences that showed polymorphism in **RFLP** analysis were used as **primers**. Optimal temperature conditions and Mg-2+ concentrations were determined for studying inter- and intraspecific DNA polymorphism in the most important cereals.

14/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09499521 BIOSIS NO.: 199497507891
Phylogenetic analysis of organellar DNA sequences in the Andropogoneae: Saccharinae.
AUTHOR: Al-Janabi S M; McClelland M; Petersen C; Sobral B W S(a)
AUTHOR ADDRESS: (a)California Inst. Biological Res., 11099 North Torrey Pines Road, Suite 300, La Jolla CA 92037**USA
JOURNAL: Theoretical and Applied Genetics 88 (8):p933-944 1994
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To study the phylogenetics of sugarcane (Saccharum officinarum L.) and its relatives we sequenced four loci on cytoplasmic genomes (two chloroplast and two mitochondrial) and analyzed mitochondrial **RFLPs** generated using probes for COXI, COXII, COXIII. Cob, 18S+5S, 26S, ATPase 6, ATPase 9, and ATPase alpha (D'Hont et al. 1993). Approximately 650 hp of DNA in the intergenic spacer region between rbcL and atpB and approximately 150 hp from the chloroplast 16S rDNA through the intergenic spacer region tRNA-val gene were sequenced. In the mitochondrial genome, part of the 18S rRNA gene and approximately 150 bp from the 18S gene 3' end, through an intergenic spacer region. to the 5S rRNA gene were sequenced. No polymorphisms were observed between maize, sorghum, and 'Saccharum complex' members for the mitochondrial 18S internal region or for the intergenic tRNA-val chloroplast locus. Two polymorphisms (insertion-deletion events, indels) were observed within the 18S-5S

mitochondrial locus, which separated the accessions into three groups: one containing all of the Erianthus, Eccoilopus, Imperata, Sorghum, and 1 Miscanthus species; a second containing Saccharum species, Narenga porphyrocoma, Scierostachya fusca, and 1 presumably hybrid Miscanthus sp. from New Guinea; and a third containing maize. Eighteen accessions were sequenced for the intergenic region between rbcL and atpB, which was the most polymorphic of the regions studied and contained 52 site mutations and 52 indels. across all taxa. Within the Saccharum complex, at most 7 site mutations and 16 indels were informative. The maternal lineage of Erianthus/Eccoilopus was nearly as divergent from the remaining Saccharum complex members as it was from sorghum, in agreement with a previous study. Sequences from the rbcL-atpB spacer were aligned with GENBANK sequences for **wheat**, rice, barley, and maize, which were used as outgroups in phylogenetic analyses. To determine whether limited intra-complex variability was caused by under sampling of taxa, we used seven restriction enzymes to digest the **PCR**-amplified rbcL-atpB spacer of an additional 36 accessions within the Saccharum complex. This analysis revealed ten restriction sites (none informative) and eight length variants (four informative). The small amount of variation present in the organellar DNAs of this polyploid complex suggests that either the complex is very young or that rates of evolution between the Saccharum complex and outgroup taxa are different. Other phylogenetic information will be required to resolve systematic relationships within the complex. Finally, no variation was observed in commercial sugarcane varieties, implying, a world-wide cytoplasmic monoculture for this crop.

14/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09395533 BIOSIS NO.: 199497403903
PCR analysis of genes encoding allelic variants of high-molecular-weight glutenin subunits at the Glu-D1 locus.
AUTHOR: D'Ovidio R(a); Porceddu E; Lafiandra D
AUTHOR ADDRESS: (a)Dip. Agrobiol. Agrochim., Univ. della Tuscia, Via S. Camillo de Lellis, 01100 Viterbo**Italy
JOURNAL: Theoretical and Applied Genetics 88 (2):p175-180 1994
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genes encoding high-molecular-weight (HMW) glutenin subunits, present in bread-**wheat** lines and cultivars, were studied by **RFLP** (restriction fragment length polymorphism) and **PCR** (**polymerase chain** reaction) analyses. In particular, allelic subunits of the xor y-type, encoded at the Glu-D1 locus present on the long arm of chromosome 1D, were investigated. The variation in size, observed in different allelic subunits, is mainly due to variation in the length of the central repetitive domain, typical of these proteins. Deletions or duplications, probably caused by unequal crossing-over, have given rise to the size heterogeneity currently observed. The possibility of using the **PCR** technique for a detailed analysis of HMW glutenin genes in order to obtain a more accurate estimation of the molecular weight of their encoded subunits, and the detection of unexpressed genes, is also described.

14/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09350704 BIOSIS NO.: 199497359074
Extraordinarily polymorphic **microsatellite** DNA in barley: Species diversity, chromosomal locations, and population dynamics.

AUTHOR: Maroof M A Saghai(a); Biyashev R M; Yang G P; Zhang Q; Allard R W
AUTHOR ADDRESS: (a)Dep. Crop Soil Environmental Sci., Virginia Polytechnic Inst. State Univ., Blacksburg, VA 24061**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (12):p5466-5470 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This study was undertaken to assess the extent of genetic variation in barley simple sequence repeats (SSRs) and to study the evolutionary dynamics of SSR alleles. SSR polymorphisms were resolved by the **polymerase chain** reaction with four pairs of **primers**. In total, 71 variants were observed in a sample of 207 accessions of wild and cultivated barley. Analyses of **wheat**-barley addition lines and barley doubled haploids identified these variants (alleles) with four loci, each located on a different chromosome. The numbers of alleles detected at a locus corresponded to the number of nucleotide repeats in the **microsatellite** sequences. The numbers of alleles at two loci were 28 and 37; to our knowledge these are the largest numbers of alleles for single Mendelian loci reported in plants. Three alleles were resolved by each of the other two loci. Allelic diversity was greater in wild than in cultivated barley and surveys of two generations (F-8 and F-53) of Composite Cross II, an experimental population of cultivated barley, showed that few of the alleles present in the 28 parents survived into generation F-53, whereas some infrequent alleles reached high frequencies. Such changes in frequency indicate that the chromosomal segments marked by the SSR alleles are under the influence of natural selection. The SSR variants allow specific DNA sequences to be followed through generations. Thus, the great resolving power of SSR assays may provide clues regarding the precise targets of natural and man-directed selection.

14/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09311099 BIOSIS NO.: 199497319469
Identification and localization of molecular markers linked to the Lr9 leaf rust resistance gene of **wheat**.
AUTHOR: Schachermayr G; Siedler H; Gale M D; Winzeler H; Winzeler M; Keller B(a)
AUTHOR ADDRESS: (a)Dep. Plant Breeding, Swiss Federal Res. Stn. Agronomy, Zurich-Reckenholz, Reckenholzstr. 191, Zu**Switzerland
JOURNAL: Theoretical and Applied Genetics 88 (1):p110-115 1994
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Near-isogenic lines (NILs) for the leaf rust resistance gene Lr9 were screened for polymorphisms at the molecular level. RAPD (random amplified polymorphic DNA) **primers** as well as **RFLP** (restriction fragment length polymorphism) markers were used. Out of 395 RAPD **primer**, tested, three showed polymorphisms between NILs, i.e., an additional band was found in resistant lines. One of these polymorphic bands was cloned and sequenced. Specific **primers** were synthesized, and after amplification only resistant lines showed an amplified product. Thus, these **primers** define a sequence-tagged site that is specific for the translocated fragment carrying the Lr9 gene. A cross between a resistant NIL and the spelt (Triticum spelta) variety 'Oberkulmer' was made, and F-2 plants were analyzed for genetic linkage. All three polymorphisms detected by the **PCR** (**polymerase chain** reaction) and one **RFLP** marker (cMWG684) showed complete linkage to

the Lr-9 gene in 156 and 133 plants analyzed, respectively. A second **RFLP** marker (PSR546) was closely linked (8 +- 2.4 cM) to the Lr-9 gene and the other four DNA markers. As this marker maps to the distal part of the long arm of chromosome 6B of **wheat**, Lr9 and the other DNA markers also map to the distal region of 6BL. All three **PCR** markers detected the Lr9 gene in independently derived breeding lines and varieties, thus proving their general applicability in **wheat** breeding programs.

14/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09266937 BIOSIS NO.: 199497275307
RFLP markers linked to the durable stem rust resistance gene Rpg1 in barley.
AUTHOR: Kilian A(a); Steffenson B J; Maroof M A Saghai; Kleinhofs A(a)
AUTHOR ADDRESS: (a)Dep. Crop Soil Sci. Genet. Cell Biol., Wash. State Univ., Pullman, WA 99164**USA
JOURNAL: Molecular Plant-Microbe Interactions 7 (2):p298-301 1994
ISSN: 0894-0282
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The gene, Rpg1, conferring stable resistance in barley to the **wheat** stem rust pathogen (Puccinia graminis f. sp. tritici) was mapped using two doubled haploid populations. Rpg1 mapped to the extreme subteleomeric region of barley chromosome 1P 0.3 and 1.1 cM proximal from the molecular markers ABG704 and plastocyanin (Plc), respectively, and 2.2 cM distal from MWG036B. The closest marker, ABG704, was sequenced and **PCR**-based markers were developed.

14/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09210537 BIOSIS NO.: 199497218907
Identification of fungi in the Gaeumannomyces-Phialophora complex by **RFLPs** of **PCR**-amplified ribosomal DNAs.
AUTHOR: Ward E(a); Akrofi A Y
AUTHOR ADDRESS: (a)Plant Pathology Dep., AFRC Inst. Arable Crops Res., Rothamsted Experimental Station, Harpenden, **UK
JOURNAL: Mycological Research 98 (2):p219-224 1994
ISSN: 0953-7562
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The **polymerase chain** reaction (**PCR**) was used to amplify ribosomal internal transcribed spacer and 5.8S DNA from isolates of Gaeumannomyces graminis, Phialophora graminicola and other root-infecting fungi, isolated mostly from cereals and grasses. Different restriction enzymes were used to digest these amplified rDNAs to find polymorphisms useful in identification. Most of the enzymes tested were useful for discriminating between G. graminis and P. graminicola, and three enzymes (Dde I, Hae III and Hha I) could be used to distinguish between the varieties of G. graminis (tritici, avenae and graminis). However, a few atypical isolates gave intermediate **RFLP** patterns. The method was found to discriminate between Gaeumannomyces-Phialophora fungi and other organisms and identify G. graminis var. tritici and P. graminicola on infected **wheat** roots. The approach is a useful addition to the techniques available for the identification of fungi in the Gaeumannomyces-Phialophora complex.

14/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09210527 BIOSIS NO.: 199497218897
Typing truffle species by **PCR** amplification of the ribosomal DNA spacers.
AUTHOR: Henrion Benedicte; Chevalier Gerard; Martin Francis(a)
AUTHOR ADDRESS: (a)Equipe de Microbiol. Forestiere, Inst. Natl. de la Recherche Agron., Cent. de Rech. de Nancy, 54**France
JOURNAL: Mycological Research 98 (1):p37-43 1994
ISSN: 0953-7562
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Variation within the internal transcribed spacer (ITS) and the intergenic spacer (IGS) of the ribosomal RNA genes of European species of Tuber was examined by **polymerase chain** reaction (**PCR**) and coupled restriction fragment length polymorphism (**RFLP**) analysis. Ribosomal DNA spacers were successfully amplified from mycelium, ectomycorrhiza, and fruit bodies of a wide range of truffle species (Tuber **aestivum**, T. albidum, T. brumale, T. excavatum, T. ferrugineum, T. magnatum, T. melanosporum, T. rufum and T. uncinatum). Interspecific variation in the length and number of restriction sites of the amplified ITS and IGS was observed and most truffles could thus be reliably distinguished by **PCR-RFLP**. In contrast, the degree of intraspecific rDNA variation observed was low within T. melanosporum, but sufficient to discriminate several isolates. These results demonstrate that the **PCR-RFLP** analysis of rDNA spacers provides an efficient alternative for typing pure fungal cultures and fruit bodies for the food industry and a versatile tool for strain fingerprinting of ectomycorrhizas in ecosystems.

14/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09209106 BIOSIS NO.: 199497217476
Evaluation of "sequence-tagged-site" **PCR** products as molecular markers in **wheat**.
AUTHOR: Talbert L E(a); Blake N K; Chee P W; Blake T K; Magyar G M
AUTHOR ADDRESS: (a)Dep. Plant Soil Sci., Montana State Univ., Bozeman, MT 59717**USA
JOURNAL: Theoretical and Applied Genetics 87 (7):p789-794 1994
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The **polymerase chain** reaction (**PCR**) is an attractive technique for many genome mapping and characterization projects. One **PCR** approach which has been evaluated involves the use of randomly amplified polymorphic DNA (RAPD). An alternative to RAPDs is the sequence-tagged-site (STS) approach, whereby **PCR** **primers** are designed from mapped low-copy-number sequences. In this study, we sequenced and designed **primers** from 22 **wheat** **RFLP** clones in addition to testing 15 **primer** sets that had been previously used to amplify DNA sequences in the barley genome. Our results indicated that most of the **primers** amplified sequences that mapped to the expected chromosomes in **wheat**. Additionally, 9 of 16 **primer** sets tested revealed polymorphisms among 20 hexaploid **wheat** genotypes when **PCR** products were digested with

restriction enzymes. These results suggest that the STS-based **PCR** analysis will be useful for generation of informative molecular markers in hexaploid **wheat**.

14/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09164445 BIOSIS NO.: 199497172815
RAPD (random amplified polymorphic DNA) analysis based intervarietal genetic relationships among hexaploid wheats.
AUTHOR: Joshi Chandrashekhar P; Nguyen Henry T(a)
AUTHOR ADDRESS: (a)Plant Molecular Genetics Lab., Dep. Agronomy Horticulure Entomology, Mail Stop 2122, Texas Tech.**USA
JOURNAL: Plant Science (Limerick) 93 (1-2):p95-103 1993
ISSN: 0168-9452
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The main objective of this study was to assess the extent of genetic diversity detected by RAPD (random amplified polymorphic DNA) technique among 15 varieties of common bread **wheat** (Triticum **aestivum** L.). The slow development of genetic linkage maps of **wheat** using conventional molecular marker strategies is attributed to the limited number of **RFLPs** (restriction fragment length polymorphisms) between **wheat** genotypes. Recently, RAPDs have been observed between closely related genotypes in several other species. We have used a set of 40 single arbitrary **primers** (10-mers) for the **PCR** (**polymerase chain** reaction)-mediated amplification of random genomic DNA fragments from wheats. Eighty percent of the **primers** yielded distinct electrophoretic profiles which could be scored. Out of 109 amplified fragments, 71 (65%) were polymorphic in these **wheat** cultivars. These results have assisted in the development of a dendrogram suggesting genetic relationships among these genotypes. Moreover, most of the spring and winter wheats were clustered together in this dendrogram based on Jaccard's coefficients. These results will be useful in the identification of suitable parents for the development of a mapping population for tagging agronomically important traits in **wheat**.

14/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09147130 BIOSIS NO.: 199497155500
Differentiation of **wheat** streak mosaic virus isolates by **PCR** and **RFLP** analysis.
AUTHOR: French Roy(a); Petrisko Jill E; Robertson Nancy L; Baenziger P Stephen
AUTHOR ADDRESS: (a)USDA, ARS, Dep. Plant Pathol., University Nebraska, Lincoln, NE**USA
JOURNAL: Phytopathology 83 (12):p1356 1993
CONFERENCE/MEETING: Joint Meeting of the American Phytopathological Society and the Society of Nematologists on Plant Pathology Beyond 2000 Nashville, Tennessee, USA November 6-10, 1993
ISSN: 0031-949X
RECORD TYPE: Citation
LANGUAGE: English

14/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09116721 BIOSIS NO.: 199497125091
Cause of tall off-types in a semidwarf spring **wheat**.
AUTHOR: Storlie E W; Talbert L E(a)
AUTHOR ADDRESS: (a)Dep. Plant Soil Sci., Mont. State Univ., Bozeman, MT 59717**USA
JOURNAL: Crop Science 33 (6):p1131-1135 1993
ISSN: 0011-183X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Tall off-types that occur in semidwarf **wheat**, Triticum **aestivum** L., cultivars may reduce grower acceptance and present problems in seed certification programs. Tall off-types occur in 'Hi-Line' spring **wheat** at a frequency of 0.20%. Segregation analysis for height indicates HiLine contained the Rht-1Rht-1rht-2rht-2 genotype. Cytological analysis of selfed progeny of the tall off-types showed a high proportion of monosomic chromosome numbers, indicating that aneuploidy may be associated with the tall off-types. Further investigation involved the use of **PCR** (**polymerase chain** reaction) with **primers** designed from clones detecting restriction fragment length polymorphism (**RFLP**) at loci on homoeologous Group 4, which contained height-reducing loci Rht-1 and Rht-2. Three sets of **primers** were used to screen progeny of tall off-types from Hi-Line. The results of this screening indicate 20% of the offspring were nullisomic for chromosome 4B. Analysis of progeny using morphological and **PCR** based screening indicate that offspring of tall off-types were 72% monosomic 4B: 8% disomic: 20% nullisomic 4B. Thus, cytological and molecular analysis reveal that Hi-Line tall off-types result from a monosomic 4B condition, which causes hemizygosity for Rht-1. Due to the random occurrence of monosomic 4B progeny from disomic semidwarf **wheat**, our results suggest that tall off-types may be an inherent and unavoidable feature of semidwarf wheats with the genotype Rht-1Rht-1rht-2rht-2.

14/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08947935 BIOSIS NO.: 199396099436
RFLP mapping of the ym4 virus resistance gene in barley.
AUTHOR: Graner A(a); Bauer E
AUTHOR ADDRESS: (a)Inst. Resistance Genetic, Federal Biol. Research Centre Agric. Forestry, Graf-Seinsheim-Str. 23,**Germany
JOURNAL: Theoretical and Applied Genetics 86 (6):p689-693 1993
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: **RFLP** (restriction fragment length polymorphism) mapping of a recessive gene (ym4) conferring resistance to barley yellow mosaic and barley mild mosaic virus was performed using progeny of 86 F-1 anther-derived doubled haploid lines. Two closely linked **RFLP** markers that flank the gene at a distance of 1.2 centiMorgans were identified. Using one of these markers (MWG10) we obtained a clear differentiation between resistant and susceptible German cultivars. An analysis of a series of unrelated barley lines with probe MWG10 did not reveal additional **RFLP** fragments. The use of this probe for both marker-assisted selection and the generation of a high-density map around the resistance locus is discussed.

14/7/14 (Item 14 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

08947934 BIOSIS NO.: 199396099435
Pre-germination genotypic screening using **PCR** amplification of half-seeds.
AUTHOR: Chunwongse J(a); Martin G B; Tanksley S D
AUTHOR ADDRESS: (a)Dep. Plant Breeding Biometry, Cornell Univ., Ithaca, NY 14853-1902**USA
JOURNAL: Theoretical and Applied Genetics 86 (6):p694-698 1993
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A simple and rapid **PCR**-based method has been developed for determining the genotype of seeds before germination. Single half-seeds of rice (Oryza sativa L.) and **wheat** (Triticum **aestivum** L. em. Thell.) were preincubated, without grinding, in an aqueous extraction buffer. The resulting supernatants were then used in **polymerase chain** reaction (**PCR**) with oligonucleotide **primers** corresponding to rice single-copy sequences or a **wheat microsatellite** repeat. **PCR** products of identical size were amplified using either the half-seed extract or DNA isolated from leaf tissue. The remnant half-seeds can be maintained in ordered arrays using microtiter plates allowing the recovery of selected genotypes. Pre-germination genotypic screening of seed populations as described in this report breeding and genetics studies.

14/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08912125 BIOSIS NO.: 199396063626
A cytogenetically based physical map of chromosome 1B in common **wheat**
AUTHOR: Kota R S; Gill K S; Gill B S(a); Endo T R
AUTHOR ADDRESS: (a)Dep. Plant Pathol., Wheat Genet. Resource Cent., Throckmorton Hall, Kans. State Univ., Manhattan**USA
JOURNAL: Genome 36 (3):p548-554 1993
ISSN: 0831-2796
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; French

ABSTRACT: We have constructed a cytogenetically based physical map of chromosome 1B in common **wheat** by utilizing a total of 18 homozygous deletion stocks. It was possible to divide chromosome 1B into 17 subregions. Nineteen **genetic markers** are physically mapped to nine subregions of chromosome 1B. Comparison of the cytological map of chromosome 1B with an **RFLP**-based genetic linkage map of Triticum tauschii revealed that the linear order of the **genetic markers** was maintained between chromosome 1B of hexaploid **wheat** and 1D of T. tauschii. Striking differences were observed between the physical and genetic maps in relation to the relative distances between the **genetic markers**. The **genetic markers** clustered in the middle of the genetic map were physically located in the distal regions of both arms of chromosome 1B. It is unclear whether the increased recombination in the distal regions of chromosome 1B is due to specific regions of increased recombination or a more broadly distributed increase in recombination in the distal regions of Triticeae chromosomes.

14/7/16 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08898555 BIOSIS NO.: 199396050056
Genetic variation and phylogenetic relationships among worldwide collections of the Russian **wheat** aphid, Diuraphis noxia (Mordvilko), inferred from allozyme and RAPD-**PCR** markers.
AUTHOR: Puterka G J(a); Black W C Vv; Steiner W M; Burton R L
AUTHOR ADDRESS: (a)USDA-ARS, Appalachian Fruit Res. Station, 45 Wiltshire Road, Kearneysville, WV 25430**USA
JOURNAL: Heredity 70 (6):p604-618 1993
ISSN: 0018-067X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genetic analyses were conducted on Diuraphis noxia (Mordvilko) populations collected from **wheat**, barley and other grasses from various countries throughout the world. These collections had been found to contain clones that differed in virulence from various cultivars, cuticular hydrocarbon profiles and life cycle characters. Discrete **genetic markers** analysed in this study included allozymes and arbitrary regions of the genome amplified by the **polymerase chain** reaction (RAPD-**PCR**). In all, 23 enzymes were evaluated 17; of these enzymes representing 20 isozyme loci, were judged suitable for allozyme analysis. Polymorphisms were detected at three (15 per cent) loci: beta-esterase (beta-EST), phosphoglucose isomerase (PGI), and 6-phosphogluconate dehydrogenase (6-PGDH). The average expected heterozygosity amongst these loci was 4.9 per cent in the worldwide collection. Allozyme variation was absent within most populations, particularly within those countries where the species was recently introduced. Much greater genetic variation was detected when populations were analysed with RAPD-**PCR**. Populations were analysed with 69 polymorphic bands amplified by seven **primers**. All populations could be distinguished with this method. Cluster analyses indicated strong similarities between U.S.A. populations and collections from South Africa, Mexico, France and Turkey. The most variation was detected among populations from the Middle East and southern Russia.

14/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08852991 BIOSIS NO.: 199396004492
Efficient characterization of biological diversity using field DNA extraction and random amplified polymorphic DNA markers.
AUTHOR: Fairbanks D J(a); Waldrigues A; Ruas C F; Ruas P M; Maughan P J; Robison L R; Andersen W R; Riede C R; Pauley C S; et al
AUTHOR ADDRESS: (a)Dep. Botany Range Sci., Brigham Young University, Provo, Utah 84602
JOURNAL: Revista Brasileira de Genetica 16 (1):p11-22 1993
ISSN: 0100-8455
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; Portuguese

ABSTRACT: DNA polymorphism analyses, such as restriction fragment length polymorphism (**RFLP**) and random amplified polymorphic DNA (RAPD) analyses, are particularly useful for genetic characterization of biological resources. We describe procedures for DNA extraction and RAPD analysis that are adapted for analyzing large numbers of samples with minimal laboratory equipment. The DNA extraction procedure reported here provided ample amounts of DNA of the purity required for **RFLP** or

RAPD analyses from various plant, animal, and protozoan species. The procedure requires relatively small amounts to tissue, does not require phenol or chloroform, and may be conducted under field conditions in the absence of running water and electricity. RAPD markers are particularly valuable when compared to **RFLPs** or isozymes since decanucleotide **primers** of arbitrary sequence tend to produce a relatively high frequency of polymorphisms per **primer** and the procedure is rapid and cost efficient. Reduction of amplification reaction volume from 25 to 15 mu-l resulted in amplified DNA markers at a 33% reduction in cost. Using quinoa (Chenopodium quinoa) genetic resources as a model, a total of 95 **primers** were initially screened on a single genotype to select those **primers** that amplified several DNA fragments that were well separated electrophoretically. Of 30 selected **primers**, 16 produced polymorphic markers among 16 randomly selected quinoa accessions. Several of these **primers** produced more than one polymorphic marker, resulting in a total of 26 polymorphisms among the 30 selected markers, indicating that polymorphic markers were relatively common and **primers** could be selected to improve efficiency in the characterization of large populations.

14/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08848605 BIOSIS NO.: 199396000106
Characterisation of **wheat**-rye recombinants with **RFLP** and **PCR** probes.
AUTHOR: Rogowsky P M; Sorrels M E; Shepherd K W; Langridge P(a)
AUTHOR ADDRESS: (a)Cent. Cereal Biotechnol., Waite Agricultural Res. Inst., Univ. Adelaide, Glen Osmond, South Aust**Australia
JOURNAL: Theoretical and Applied Genetics 85 (8):p1023-1028 1993
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The introgression of genetic material from alien species into **wheat** has become an important tool in modern **wheat** breeding. Ideally, only the trait of interest and no flanking material should be transferred. Random recombination between the genetic material is therefore of paramount importance. In a model system, we examined 17 recombinants putatively between chromosome 1D of **wheat** and 1R of rye (Secale cereale) with 60 random **RFLP** and three **PCR** markers. The recombinants had been generated by removing the normal effect of the Ph1 gene in the **wheat** background. Amongst the nine short-arm recombinants, three breakpoints were identified but no differentiation could be made between the five proximal recombinants. For the eight long-arm recombinants analysed only two breakpoints were identified with 36 markers. However, only a single **RFLP** marker was able to differentiate between the recombinants. Indeed the long-arm results are consistent with the possibility that only the rye telomeric region had been transferred. These results indicate either a strong clustering of the **RFLP** markers near the centromere or else imply that recombination induced between **wheat** and rye in the absence of the normal effect of the Ph1 gene occurs at only restricted sites. The results allow new primary recombinants to be selected for intercrossing to generate secondary recombinants which are expected to have a smaller interstitial rye segment than that present in DR-A1.

14/7/19 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08826234 BIOSIS NO.: 199395115585

Pedigree assessment using RAPD-DGGE in cereal crop species.
AUTHOR: Dweikat Ismail(a); MacKenzie Sally; Levy Morris; Ohm Herbert
AUTHOR ADDRESS: (a)Dep. Agron., Purdue Univ., West Lafayette, IN 47907**USA
JOURNAL: Theoretical and Applied Genetics 85 (5):p497-505 1993
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The introduction of molecular biology methodologies to plant improvement programs offers an invaluable opportunity for extensive germplasm characterization. However, the detection of adequate DNA polymorphism in self-pollinating species remains on obstacle. We have optimized a denaturing-gradient-gel-electrophoresis (DGGE) system which, when used in combination with random amplified polymorphic DNA (RAPD) analysis, greatly facilitates the detection of reproducible DNA polymorphism among closely related plant lines. We have used this approach to estimate pedigree relationships among a spectrum of plant materials in **wheat**, barley and oat. (Triticum **aestivum**, Hordeum vulgare, Avena sativa). Based on analysis with one or two **primers**, we were able to distinguish soft from hard winter **wheat**, and 2-rowed from 6-rowed barley. Further analysis with additional **primers** allowed resolution of polymorphisms even among closely related lines in highly selected populations. We placed 17 cultivars of oat into two distinct clusters that differed significantly from previous oat pedigree assessments. We believe that DGGE-RAPD is a superior method for detecting DNA polymorphism when compared to **RFLP**, agarose-RAPD, or polyacrylamide-RAPD methods.

14/7/20 (Item 20 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08402637 BIOSIS NO.: 000094120291
THE USE OF RANDOM AMPLIFIED POLYMORPHIC DNA MARKERS IN **WHEAT**
AUTHOR: DEVOS K M; GALE M D
AUTHOR ADDRESS: CAMBRIDGE LAB., COLNEY LANE, NORWICH NR4 7UJ, UK.
JOURNAL: THEOR APPL GENET 84 (5-6). 1992. 567-572.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An evaluation was made of the use of random amplified polymorphic DNA (RAPD) as a **genetic marker** system in **wheat**. Reproducible amplification products were obtained from varietal, homozygous single chromosome recombinant line and **wheat**/alien addition line genomic DNA with selected **primers** and rigorously optimized reaction conditions. Factors influencing the RAPD patterns are DNA concentrations, Mg2+ concentration, polymerase concentration and denaturing temperature. In **wheat**, the non-homoeologous, non-dose responsive and dominant behaviour of RAPD products devalues their use as **genetic markers** for the construction of linkage maps, and the high probability that the amplified fragments derive from repetitive DNA limits their use as a source of conventional **RFLP** probes. However, RAPD markers will most certainly find many applications in the analysis of genotypes where single chromosomes or chromosomes segments are to be manipulated.

14/7/21 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08312027 BIOSIS NO.: 000094074350

USE OF THE RANDOM AMPLIFIED POLYMORPHIC DNA **POLYMERASE CHAIN** REACTION RAPD-**PCR** TO DETECT DNA POLYMORPHISMS IN APHIDS HOMOPTERA APHIDIDAE

AUTHOR: BLACK W C IV; DUTEAU N M; PUTERKA G J; NECHOLS J R; PETTORINI J M
AUTHOR ADDRESS: DEP. ENVIRONMENTAL HEALTH, COLO. STATE UNIV., FORT COLLINS, COLO. 80525.

JOURNAL: BULL ENTOMOL RES 82 (2). 1992. 151-159.
FULL JOURNAL NAME: Bulletin of Entomological Research
CODEN: BEREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have used a new technique to identify discrete **genetic markers** in aphids, a family in which biochemical and morphological genetic polymorphisms are rare. The new technique uses the **polymerase chain** reaction (**PCR**) to amplify random regions of aphid genomes (random amplified polymorphic DNA) and has been termed RPAD-**PCR**. We demonstrate the use of the technique in revealing genetic variation in four aphid species, the greenbug (Schizaphis graminum (Rondani)), the Russian **wheat** aphid (Diuraphis noxia (Mordvilko)), the pea aphid (Acyrthosiphon pisum (Harris)), and the brown ambrosia aphid (Uroleucon ambrosiae (Thomas)). In contrast with allozyme surveys, RAPD-**PCR** revealed large amounts of genetic variation among individuals in each of these species. Variation was detected among biotypes, populations, colour morphs and even individuals on a single plant. We also explored the utility of RAPD-**PCR** in the detection and identification within aphid bodies of two endoparasitic wasps, Diaeretiella rapae (McIntosh) and Lysiphlebus testaceipes (Cresson). The use of RAPD-**PCR** in species diagnostics, parasitoid detection, and population studies is discussed.

14/7/22 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08290925 BIOSIS NO.: 000094062223
RFLP AND **PCR** ANALYSES AT GLI-1 GLI-2 GLU-1 AND GLU-3 LOCI IN CULTIVATED AND WILD WHEATS

AUTHOR: D'OVIDIO R; TANZARELLA O A; MASCI S; LAFIANDRA D; PORCEDDU E
AUTHOR ADDRESS: DIP. AGROBIOLOGIA AGROCHIMICA, UNIVERSITA STUDI TUSCIA, 01100 VITERBO, ITALY.

JOURNAL: HEREDITAS 116 (1-2). 1992. 79-85.
FULL JOURNAL NAME: Hereditas
CODEN: HEREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: **RFLP** and **PCR** analyses at the Gli-1, Gli-2, Glu-1 and Glu-3 loci have been carried out in Aegilops L. and Triticum L. species. High level of polymorphism was found by **RFLP** analyses both between Aegilops species and Triticum species, and between durum **wheat** cultivars, whereas **PCR** analyses of the coding region of the same genotypes showed a different degree of variation between the analyzed loci. Gamma gliadin amplified products revealed a moderate level of polymorphism between Aegilops and Triticum species, and showed the possibility of distinguishing durum **wheat** cultivars with good and poor technological properties. **PCR** products of alpha/beta gliadins and low (LMW) and high molecular weight (HMW) glutenins showed a low degree of variation between Aegilops and Triticum species. Finally, **RFLP** analysis at the Gli-2 locus of Aegilops species has shown that it is possible to differentiate the Ae. squarrosa subsp. strangulata from the Ae. squarrosa subsp. squarrosa, and suggests introgression from Ae. longissima or Ae. searsii into tetraploid and hexaploid Ae. crassa, Ae. juvenalis, and Ae. vavilovii.

14/7/23 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07841947 BIOSIS NO.: 000092112113
IDENTIFICATION AND MAPPING OF POLYMORPHISMS IN CEREALS BASED ON THE **POLYMERASE CHAIN** REACTION
AUTHOR: WEINING S; LANGRIDGE P
AUTHOR ADDRESS: CENTRE CEREAL BIOTECHNOL., WAITE AGRIC. RES. INST., UNIV. ADELAIDE, GLEN OSMOND, S. AUST. 5064, AUST.
JOURNAL: THEOR APPL GENET 82 (2). 1991. 209-216.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The **polymerase chain** reaction (**PCR**) can be used to detect polymorphisms in the length of amplified sequences between the annealing sites of two synthetic DNA **primers**. When the distance varies between two individuals then the banding pattern generated by the **PCR** reaction is essentially a genetic polymorphism and can be mapped in the same way as other **genetic markers**. This procedure has been used in a number of eukaryotes. Here we report the use of **PCR** to detect genetic polymorphism in cereals. Known gene sequences can be used to design **primers** and detect polymorphic **PCR** products. This is demonstrated with **primers** to the .alpha.-amylase gene family. A second approach is to use semi-random **primers** to target diverse regions of the genome. For this purpose the consensus sequences at the intron-exon splice junctions were used. The targeting of the intron-exon splice junctions in conjunction with **primers** of random and defined sequences, such as .alpha.-amylase, provides a source of extensive variation in **PCR** products. These polymorphisms can be mapped as standard **genetic markers**.

14/7/24 (Item 24 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07319369 BIOSIS NO.: 000090099269
RAPID AND EFFICIENT DETECTION OF GENETIC POLYMORPHISM IN **WHEAT** THROUGH AMPLIFICATION BY **POLYMERASE CHAIN** REACTION
AUTHOR: D'OVIDIO R; TANZARELLA O A; PORCEDDU R
AUTHOR ADDRESS: DIPARTIMENTO DI AGROBIOLOGIA E AGROCHIMICA, UNIVERSITA DELLA TUSCIA, VIA S. CAMILLO DE LELLIS, 001100 VITERBO, ITALY.
JOURNAL: PLANT MOL BIOL 15 (1). 1990. 169-172.
FULL JOURNAL NAME: Plant Molecular Biology
CODEN: PMBID
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The **polymerase chain** reaction (**PCR**) was used to amplify genomic DNA of several **wheat** [Triticum] genotypes. The oligonucleotides used as **primers** were the terminal sequences of a gamma-gliadin gene. The electrophoretic analysis of the **PCR** products showed specific bands which revealed both inter- and intra-specific genetic polymorphism among the examined genotypes. The technique is proposed as a very simple and efficient alternative to **RFLP** markers.

14/7/25 (Item 1 from file: 35)
DIALOG(R)File 35:DISSERTATION ABSTRACTS ONLINE

01351713 ORDER NO: AAD94-12502
EVOLUTION AND RETROTRANSPOSITION IN THE TRITICEAE
Author: MONTE HERRAIZ, JUAN VICENTE
Degree: PH.D.
Year: 1993
Corporate Source/Institution: UNIVERSITY OF MISSOURI - COLUMBIA (0133)
Supervisor: J. P. GUSTAFSON
Source: VOLUME 54/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 5502. 121 PAGES

The use of restriction fragment length polymorphisms (**RFLPs**) in combination with other approaches is very useful for the reconstruction of evolutionary events revealing phylogenetic relationships. A set of cDNA probes was used in a series of experiments designed to estimate the phylogenetic relationships among and within 16 species of the Triticeae tribe. The **RFLP** data were used to generate both a cladogram and a phenogram in order to compare the two different methods of constructing phylogenetic trees. The results were consistent with the general taxonomic information provided by previous taxonomic analyses. However, a close association between the P and R genomes was observed that only had been reported before in studies of sequence alignment in the Ter locus. The association between the S and N was consistent with previous isozyme analyses. In addition, several significant correlations were found between accessions of the same species from different geographical origins and their phylogenetic relationships as shown by the cladogram and phenogram.

WIS 2-1A, the first retrotransposon found in **wheat**, has been recently studied and characterized. Regarding the potential dramatic impact that transposable elements may have in genomic evolution, WIS 2-1A was studied utilizing several species from the Triticeae. Southern hybridization experiments revealed the presence of homologous sequences in all the taxa tested, showing high levels of interspecific variability and almost no intraspecific differentiation. Further experiments using in situ hybridization in several species showed that the retroposon was almost completely disperse throughout the genomes tested. These results suggested that WIS 2-1A is an ancient element that probably was present in the unknown common ancestor of the Triticeae and only under rare circumstances becomes active. The dispersion shown by the in situ experiments supports the idea that WIS 2-1A does not have preferential insertion targets. Finally, DNA fragments homologous to the WIS 2-1A Reverse Transcriptase gene were isolated in most of the Triticeae species using **PCR**. The fragments obtained were sequenced and analyzed. Even though the sequence alignment was consistent with the phylogenetic relationships analyzed in the first part of the project, in the case of the genus Thinopyrum evidence for a possible horizontal propagation of the retroelement was observed.

14/7/26 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

05479206 EMBASE No: 1993247305
Application of the random amplified polymorphic DNA technique for the detection of polymorphism among wild and cultivated tetraploid wheats
Joshi C.P.; Nguyen H.T.
Plant Molecular Genetics Laboratory, Dept.
Agronomy,Horticulture/Entomol., Texas Tech University,Lubbock, TX 79409 United States
Genome (GENOME) (Canada) 1993, 36/3 (602-609)
CODEN: GENOE ISSN: 0831-2796
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Development of a high-density genetic linkage map of cultivated wheats using conventional molecular markers has lagged behind the other major foodcrops such as rice and tomato because of the large genome size and limited levels of genetic polymorphisms. Recently, random amplified

polymorphic DNAs (RAPDs) have been suggested to provide an alternative to visualize more polymorphism. For the construction of a genetic linkage map in tetraploid wheats, one can use a strategy of intersubspecific crosses between the most dissimilar wild and cultivated tetraploid wheats that are easy to hybridize and result in fertile progeny. An assessment of the level of RAPDs among different accessions and varieties of wild and cultivated tetraploid wheats is required to fulfill this objective. We present here the data obtained using RAPD analysis of 40 **primers** in 20 accessions of wild tetraploid emmer wheats (Triticum turgidum L. ssp. dicoccoides) and 10 genotypes of cultivated tetraploid durum wheats (Triticum turgidum L. ssp. durum) selected from geographically diverse locations. We have observed a higher level of polymorphism among different accessions of wild emmer **wheat** from Israel, Turkey, and Jordan than the group of cultivated American, Turkish, and Syrian durum wheats. These data have been used to generate a dendrogram suggesting the genetic relationships among these genotypes, and the most dissimilar genotypes are identified for future mapping and gene tagging work.

14/7/27 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07938468 94282093
An approach towards genetically engineered cell fate mapping in maize using the Lc gene as a visible marker: transactivation capacity of Lc vectors in differentiated maize cells and microinjection of Lc vectors into somatic embryos and shoot apical meristems.
Lusardi MC; Neuhaus-Url G; Potrykus I; Neuhaus G
Institute of Plant Sciences, Swiss Federal Institute of Technology, Zurich.
Plant J (ENGLAND) Apr 1994, 5 (4) p571-82, ISSN 0960-7412
Journal Code: BRU
Languages: ENGLISH
Document type: JOURNAL ARTICLE
To establish a system for genetically engineered cell fate mapping, different vectors carrying the Lc gene, a member of the R gene family, were delivered into embryonic and meristematic cells of maize by the microinjection technique. Vectors in which the Lc cDNA is driven either by a constitutive promoter (CaMV 35S), with or without the Adh1 intron 1 of maize, or a tissue-specific promoter (phosphoenolpyruvate carboxylase, PEPC) as well as self-replicating **wheat** dwarf virus (WDV) vectors carrying a Lc-expression-cassette, have been tested. The ability of these vectors to transactivate was evaluated in mesophyll-derived protoplasts of the maize genotype appropriate for these microinjection experiments. The expression product of the introduced Lc gene can substitute for mutated R and B loci, resulting in anthocyanin production. Analogous results were obtained by microinjection into organized tissues, where transactivation of anthocyanin biosynthesis resulted in pigmented sectors in somatic embryos (B79) and in the leaves of plants regenerated from the cultivated shoot apical meristems (K55, r-g, b). The tissue-specific appearance of pigmented sectors in leaves, using the mesophyll-specific PEPC promoter suggests the possibility of using this approach for layer-specific cell fate studies. The presence of the introduced plasmids in leaves showing red sectors 20-30 days after injection was proven by **PCR** analysis.

14/7/28 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07925528 94261606
Extraordinarily polymorphic **microsatellite** DNA in barley: species diversity, chromosomal locations, and population dynamics.
Saghai Maroof MA; Biyashev RM; Yang GP; Zhang Q; Allard RW
Department of Crop and Soil Environmental Sciences, Virginia Polytechnic

Institute and State University, Blacksburg 24061.
Proc Natl Acad Sci U S A (UNITED STATES) Jun 7 1994, 91 (12) p5466-70, ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: JOURNAL ARTICLE
This study was undertaken to assess the extent of genetic variation in barley simple sequence repeats (SSRs) and to study the evolutionary dynamics of SSR alleles. SSR polymorphisms were resolved by the **polymerase chain** reaction with four pairs of **primers**. In total, 71 variants were observed in a sample of 207 accessions of wild and cultivated barley. Analyses of **wheat**-barley addition lines and barley doubled haploids identified these variants (alleles) with four loci, each located on a different chromosome. The numbers of alleles detected at a locus corresponded to the number of nucleotide repeats in the **microsatellite** sequences. The numbers of alleles at two loci were 28 and 37; to our knowledge these are the largest numbers of alleles for single Mendelian loci reported in plants. Three alleles were resolved by each of the other two loci. Allelic diversity was greater in wild than in cultivated barley and surveys of two generations (F8 and F53) of Composite Cross II, an experimental population of cultivated barley, showed that few of the alleles present in the 28 parents survived into generation F53, whereas some infrequent alleles reached high frequencies. Such changes in frequency indicate that the chromosomal segments marked by the SSR alleles are under the influence of natural selection. The SSR variants allow specific DNA sequences to be followed through generations. Thus, the great resolving power of SSR assays may provide clues regarding the precise targets of natural and man-directed selection.

14/7/29 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07887320 94198897
Fertile transgenic **wheat** from microprojectile bombardment of scutellar tissue.
Becker D; Brettschneider R; Lorz H
Zentrum fur Angewandte Molekularbiologie der Pflanzen, AMP II, Institut fur Allgemeine Botanik der Universitat, Hamburg, Germany.
Plant J (ENGLAND) Feb 1994, 5 (2) p299-307, ISSN 0960-7412 Journal Code: BRU
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A reproducible transformation system for hexaploid **wheat** was developed based on particle bombardment of scutellar tissue of immature embryos. Particle bombardment was carried out using a PDS 1000/He gun. Plant material was bombarded with the plasmid pDB1 containing the beta-glucuronidase gene (uidA) under the control of the actin-1 promoter of rice, and the selectable marker gene bar (phosphinothricin acetyltransferase) under the control of the CaMV 35S promoter. Selection was carried out using the herbicide Basta (Glufosinate-ammonium). From a total number of 1050 bombarded immature embryos, in seven independent transformation experiments, 59 plants could be regenerated. Putative transformants were screened for enzyme activity by the histochemical GUS assay using cut leaf material and by spraying the whole plants with an aqueous solution of the herbicide Basta. Twelve regenerants survived Basta spraying and showed GUS-activity. Southern-blot analysis indicated the presence of introduced foreign genes in the genomic DNA of the transformants and both marker genes were present in all plants analysed. To date, four plants have been grown to maturity and set seed. Histochemically stained pollen grains showed a 1:1 segregation of the uidA gene in all plants tested. A 3:1 segregation of the introduced genes was demonstrated by enzyme activity tests and Southern blot analysis of R1 plants.

14/7/30 (Item 1 from file: 10)

DIALOG(R)File 10:AGRICOLA

3415522 20436218 Holding Library: AGL
Identification of glutenin alleles in **wheat** and triticale using **PCR**-generated DNA markers
Smith, R.L. Schweder, M.E.; Barnett, R.D.
North Florida Res. & Ed. Ctr., Quincy, FL.
Madison, Wis. : Crop Science Society of America, 1961-
Crop science. Sept/Oct 1994. v. 34 (5) p. 1373-1378.
ISSN: 0011-183X CODEN: CRPSAY
DNAL CALL NO: 64.8 C883
Language: English
Includes references
Place of Publication: Wisconsin
Subfile: IND; OTHER US (NOT EXP STN, EXT, USDA; SINCE 12/76);
Document Type: Article
Quality in **wheat** (Triticum **aestivum** L. em Thell.) is a very complex trait; however, the water insoluble gluten proteins are responsible for the elasticity and cohesiveness (strength) of dough and are important determinants of breadmaking quality. High molecular weight glutenin subunits encoded by genes on the long arms of Group I chromosomes have been associated with gluten strength, and a portion of the variability between cultivars can be attributed to glutenin subunit composition. Of the glutenins. Subunits 5 + 10 encoded by the D genome have been found to have the largest positive effect on dough strength, whereas the allelic Subunits 2 + 12 have a negative effect. Therefore, it has been important to incorporate the genes for the 5 + 10 subunits into bread wheats. There has been considerable interest in improving the dough strength and quality of soft wheats and triticale (X Tritico secale Whittm.) to use them in bread-like products. Glutenin subunit screening is accomplished using electrophoresis (SDS-PAGE). In this paper, we report the development of an alternative screening method based on the glutenin genes themselves, using the **polymerase chain** reaction (**PCR**). **Primers** designed from computer analyses were synthesized and tested on the cloned subunit 10 gene (Glu-D1-2b), 10 **wheat** cultivars of known subunit composition, and six triticales. Although the Glu-D1-2b (Dy10) and Glu-D1-2a (Dy12) genes have 98.9% DNA sequence similarity, marker fragments capable of consistently identifying those genotypes were amplified. Fragments correlating with glutenin subunit composition offering possibilities of extending the **PCR** screening system to other subunits were noted.

14/7/31 (Item 2 from file: 10)
DIALOG(R)File 10:AGRICOLA

3415422 20436115 Holding Library: AGL
Increase of inheritance polymorphisms of arbitrary primed **PCR** products on DGGE gels
Procunier, J.D. Wolf, M.; Howes, N.K.
Agriculture and Agri-Food Canada, Manitoba, Canada.
Middlesex, England : Science & Technology Letters.
Biotechnology techniques. Oct 1994. v. 8 (10) p. 707-710.
ISSN: 0951-208X CODEN: BTECE6
DNAL CALL NO: TP248.24.B55
Language: English
Includes references
Place of Publication: England
Subfile: IND; OTHER FOREIGN;
Document Type: Article

14/7/32 (Item 3 from file: 10)
DIALOG(R)File 10:AGRICOLA

3394906 20419211 Holding Library: AGL
Russian **wheat** aphid resistance in barley: inheritance and linked molecular markers
Nieto-Lopez, R.M. Blake, T.K.
Madison, Wis. : Crop Science Society of America, 1961-
Crop science. May/June 1994. v. 34 (3) p. 655-659.
ISSN: 0011-183X CODEN: CRPSAY
DNAL CALL NO: 64.8 C883
Language: English
Includes references
Place of Publication: Wisconsin
Subfile: IND; OTHER US (NOT EXP STN, EXT, USDA; SINCE 12/76);
Document Type: Article

Russian **wheat** aphid (RWA), Diuraphis noxia (Mordvilko), is an important pest of small grains cereals in many areas throughout the world. This research was conducted to determine the inheritance of resistance and to identify molecular markers of resistance in the barley (Hordeum vulgare L.) lines PI366444 and PI366453. Artificial infestation was performed in the field and growth chamber. Sodium dodecyl sulphate-polyacrylamide gel electrophoresis, Southern blotting, and **polymerase chain** reaction (**PCR**) techniques were used to determine plant genotypes. The PI366444 and PI366453 lines were intercrossed and each was also crossed with the susceptible cultivars Stark and Bearpaw. Allelism tests of F2 progeny showed that the resistant lines shared common or tightly linked resistance genes. Segregation ratios from crosses among resistant and susceptible plants, measured using families, indicated that there were at least two resistance genes in both of the PI lines. Two different regions in the barley genome were associated with RWA resistance genes. Variation for both leaf chlorosis and leaf rolling in F2 plants from crosses with both resistant lines was associated with the sequence-tagged-site (STS) **PCR** markers B-hordein and D14 on the short arm of Chromosome 5. The STS-**PCR** marker ABG8 on Chromosome 2 was associated with leaf rolling in one cross. Barley breeding programs throughout North America have devoted significant time and resources to backcrossing RWA resistance genes into acceptable cultivars. The molecular markers described in this report may assist barley breeding programs in introgression and fixation of linked resistance genes into useful germplasm.

14/7/33 (Item 4 from file: 10)
DIALOG(R)File 10:AGRICOLA

3285643 93030578 Holding Library: AGL
Analysis of single protoplasts and regenerated plant by **PCR** and RAPD technology
Brown, P.T.H. Lange, F.D.; Kranz, E.; Lorz, H.
Institut fur Allgemeine Botanik, Hamburg, FRG
Berlin, W. Ger. : Springer International.
M G G : Molecular and general genetics. Mar 1993. v. 237 (3) p. 311-317.
ISSN: 0026-8925 CODEN: MGGEAE
DNAL CALL NO: 442.8 Z34
Language: English
Includes references.
Subfile: OTHER FOREIGN;
Document Type: Article

We investigated the use of the **polymerase chain** reaction (**PCR**) and the associated random amplification of polymorphic DNA (RAPD) technique in the analysis of DNA and specific genes in plant cells at different stages of regeneration in in vitro cultures. We demonstrate that both procedures can be used to differentiate reproducibly between closely related species as well as to reveal levels of DNA polymorphism in regenerated plants. We also demonstrate that both procedures, using protocols that we have developed, are applicable at all tissue culture

stages, from single isolated protoplasts to regenerated plants. Possible explanations for the variation levels detected in regenerated **wheat** plants are advanced.

14/7/34 (Item 5 from file: 10)
DIALOG(R)File 10:AGRICOLA

3277493 93024105 Holding Library: AGL
Characteristics of **wheat**-rye recombinants with **RFLP** and **PCR** probes
Rogowsky, P.M. Sorrels, M.E.; Shepherd, K.W.; Langridge, P.
The University of Adelaide, Glen Osmond, South Australia
Berlin, W. Ger. : Springer International.
Theoretical and applied genetics. Feb 1993. v. 85 (8) p. 1023-1028.
ISSN: 0040-5752 CODEN: THAGA
DNAL CALL NO: 442.8 Z8
Language: English
Includes references.
Subfile: OTHER FOREIGN;
Document Type: Article
The introgression of genetic material from alien species into **wheat** has become an important tool in modern **wheat** breeding. Ideally, only the trait of interest and no flanking material should be transferred. Random recombination between the genetic material is therefore of paramount importance. In a model system, we examined 17 recombinants putatively between chromosome 1D of **wheat** and 1R of rye with 60 random **RFLP** and three **PCR** markers. The recombinants had been generated by removing the normal effect of the Ph1 gene in the **wheat** background. Amongst the nine short-arm recombinants, three breakpoints were identified but no differentiation could be made between the five proximal recombinants. For the eight long-arm recombinants analysed only two breakpoints were identified with 36 markers. However, only a single **RFLP** marker was able to differentiate between the recombinants. Indeed the long-arm results are consistent with the possibility that only the rye telomeric region had been transferred. These results indicate either a strong clustering of the **RFLP** markers near the centromere or else imply that recombination induced between **wheat** and rye in the absence of the normal effect of the Ph1 gene occurs at only restricted sites. The results allow new primary recombinants to be selected for intercrossing to generate secondary recombinants which are expected to have a smaller interstitial rye segment than that present in DR-A1.

14/7/35 (Item 6 from file: 10)
DIALOG(R)File 10:AGRICOLA

3232993 92069553 Holding Library: AGL
Use of RAPD markers to determine the genetic diversity of diploid, **wheat** genotypes
Vierling, R.A. Nguyen, H.T.
Indiana Crop Improvement, Lafayette, IN
Berlin, W. Ger. : Springer International.
Theoretical and applied genetics. Sept 1992. v. 84 (7/8) p. 835-838.
ISSN: 0040-5752 CODEN: THAGA
DNAL CALL NO: 442.8 Z8
Language: English
Includes references.
Subfile: OTHER FOREIGN;
Document Type: Article
The genetic diversity of two diploid **wheat** species, Triticum monococcum and Triticum urartu (2n = 2x = 14), was assessed using random **primers** and the **polymerase chain** reaction (**PCR**). Electrophoretic analysis of the amplification products revealed a higher

incidence of polymorphism in T. urartu than T. monococcum. Pair-wise comparisons of unique and shared polymorphic amplification products, were used to generate Jaccard's similarity coefficients. These were employed to construct phenograms using an unweighted pair-group method with arithmetical averages (UPGMA). The UPGMA analysis indicated a higher similarity among T. monococcum than T. urartu. Analysis of RAPD data appears to be helpful in determining the genetic relationships among genotypes.

14/7/36 (Item 7 from file: 10)
DIALOG(R)File 10:AGRICOLA

3220776 92060264 Holding Library: AGL
Detection of DNA sequence polymorphisms among **wheat** varieties
He, S. Ohm, H.; Mackenzie, S.
Purdue University, West Lafayette, IN
Berlin, W. Ger. : Springer International.
Theoretical and applied genetics. 1992. v. 84 (5/6) p. 573-578.
ISSN: 0040-5752 CODEN: THAGA
DNAL CALL NO: 442.8 Z8
Language: English
Includes references.
Subfile: OTHER FOREIGN;
Document Type: Article
A DNA marker detection strategy that allows the rapid, efficient resolution of high levels of polymorphism among closely related lines of common **wheat** (Triticum **aestivum**) has been developed to circumvent the apparent lack of restriction fragment length polymorphism in many important self-pollinated crop species. The technique of randomly amplified polymorphic DNA (RAPD) was combined with a denaturing gradient gel electrophoresis system (DGGE) to explore DNA sequence polymorphisms among different genotypes of **wheat**. Of the 65 **primer** combinations used for the **polymerase chain** reaction (**PCR**) amplifications, over 38% of them produced readily detectable and reproducible DNA polymorphisms between a spring **wheat** line, SO852, and a winter **wheat** variety, 'Clark'. A high level of polymorphism was observed among a number of commercial varieties and breeding lines of **wheat** . This procedure was also used to detect polymorphisms in a recombinant inbred population to test the feasibility of its application in genome mapping. This DNA polymorphism detection system provides an opportunity for pedigree analysis and fingerprinting of developed **wheat** lines as well as construction of a high density genetic map of **wheat** . Without the need for 32P and sophisticated DNA extraction procedures, this approach should make it feasible to utilize marker-based selection in a plant breeding program.

14/7/37 (Item 1 from file: 203)
DIALOG(R)File 203:AGRIS

02141796 AGRIS No: 97-091100
PCR analysis of genes encoding allelic variants of high-molecular-weight glutenin subunits at the Glu-D1 locus
Ovidio, R. de; Porceddu, E.; Lafiandra, D. (Tuscia Univ., Viterbo (Italy). Dept. di Agrobiologia e Agrochimica)
Journal: Theoretical and Applied Genetics, 1994, v. 88(2) p. 175-180
Notes: 4 ill., 1 graph, 2 tables; 23 ref. ISSN: 0040-5752
Language: English Summary Language: English
Place of Publication: Germany
Document Type: Journal Article, Summary
Journal Announcement: 2307 Record input by Germany
Abstract in English
Genes encoding high-molecular-weight (HMW) glutenin subunits, present in

bread-**wheat** lines and cultivars, were studied by **RFLP** (restriction fragment length polymorphism) and **PCR** (**polymerase chain** reaction) analyses. In particular, allelic subunits of the x- or y-type, encoded at the Glu-D1 locus present on the long arm of chromosome 1D, were investigated. The variation in size, observed in different allelic subunits, is mainly due to variation in the length of the central repetitive domain, typical of these proteins. Deletions or duplications, probably caused by unequal crossing-over, have given rise to the size heterogeneity currently observed. The possibility of using the **PCR** technique for a detailed analysis of HMW glutenin genes in order to obtain a more accurate estimation of the molecular weight of their encoded subunits, and the detection of unexpressed genes, is also described.

14/7/38 (Item 2 from file: 203)
DIALOG(R)File 203:AGRIS

02000686 AGRIS No: 96-081346
Genetics, **markers**, maps and **wheat** breeding
Gale, M.D. (John Innes Centre, Colney Lane, Norwich NR4 7UH (United Kingdom))
Journal: Journal of the Royal Agricultural Society of England, 1994, v. 155 p. 162-176
Notes: 25 ref.
Language: English
Place of Publication: United Kingdom
Document Type: Journal Article,
Journal Announcement: 2207 Record input by United Kingdom

14/7/39 (Item 3 from file: 203)
DIALOG(R)File 203:AGRIS

01904989 AGRIS No: 95-111359
Genetic analysis with RAPD markers in **wheat** (Analisis genetico con marcadores moleculares de secuencias de ADN amplificadas (RAPD) en trigo)
Barriga B, Patricio (Universidad Austral de Chile, Valdivia (Chile). Fac. de Ciencias Agrarias); Slebe T, Juan C.; Mansilla S, Jorge
Journal: Agro Sur, Jul-Dic 1994, v. 22(2) p. 133-142
Notes: 12 ref. ISSN: 0304-8802
Language: Spanish Summary Language: English, Spanish
Place of Publication: Chile
Document Type: Journal Article, Summary
Journal Announcement: 2110 Record input by Chile
Abstract in Espanol
Recientemente se ha comenzado a utilizar los marcadores moleculares de secuencias de ADN amplificadas (RAPD) como una tecnica para la caracterizacion de germoplasma y para estimar las relaciones geneticas entre individuos en estudios de poblaciones intraespecificos, en muchas especies cultivadas. En este trabajo se establecio un protocolo para la aplicacion de la tecnologia de los RAPD a los analisis geneticos en trigo. Con dicho protocolo fue posible obtener ADN genomico varietal, de alto peso molecular y la amplificacion de los polimorfos con **primers** seleccionados, haciendo posible la diferenciacion de variedades de trigo. Las variaciones en las condiciones de amplificacion, tales como la concentracion de ADN, la concentracion de Mg2+, los tiempos de los ciclos de apareamiento y de polimerizacion, fueron parametros importantes en el analisis de RAPD para trigo.

14/7/40 (Item 4 from file: 203)
DIALOG(R)File 203:AGRIS

01834150 AGRIS No: 95-012770
RAPDs [random amplified polymorphic DNA] as molecular markers for the detection of the presence of rye chromosomes in **wheat** (RAPD [random amplified polymorphic DNA] come marcatori molecolari per l'individuazione della presenza di cromosomi di segale nel frumento)
Koebner, R.M.D.; Martin, P.K.
Journal: Journal of Genetics and Breeding, Mar 1994, v. 48(1) p. 85-88
Notes: 1 table; 1 graph; 18 ref. ISSN: 0394-9257
Language: English Summary Language: English
Place of Publication: Italy
Document Type: Journal Article, Summary
Journal Announcement: 2102 Record input by Italy
Abstract in English, Italiano
The RAPD-**PCR** technique was explored as a source of convenient markers for the presence of rye chromosomes/chromosome segments present in a **wheat** background. Although a large number of **primers** gave differential rye **PCR** products in the **wheat** x rye hybrids tested, many of these patterns were not reproducible; of those that were reliable, the majority did not amplify the rye product from template carrying only one pair of rye chromosomes. Where the assay was successful in distinguishing addition lines from euploid template, in all but one case, more than one rye chromosome carried the appropriate **primer** annealing sites.

[La tecnica RAPD-**PCR** e' stata indagata come fonte di marcatori utili per la presenza di cromosomi/segmenti di cromosomi di segale nel grano. Sebbene un ampio numero di iniettori abbiano fornito prodotti **PCR** di segale differenziali negli ibridi di grano x segale testati, molti di questi modelli non erano riproducibili. Di quelli affidabili, la maggior parte non amplificava il prodotto di segale da uno stampo che porta solo una coppia di cromosomi di segale. Dove la prova ha distinto con successo le linee aggiuntive dallo stampo euploide, in tutti i casi, eccetto uno, piu' di un cromosoma di segale portava i siti appropriati].

14/7/41 (Item 5 from file: 203)
DIALOG(R)File 203:AGRIS

01834147 AGRIS No: 95-012767
Development of DNA markers based on randomly amplified polymorphic sequences in a Triticum **aestivum** L. x Thinopyrum bessarabicum amphiploid (Sviluppo dei marcatori DNA in base alle sequenze polimorfiche amplificate randomizzate in un anfiploide Triticum **aestivum** L. x Thinopyrum bessarabicum)
William, M.D.H.M.; Mujeeb Kazi, A. (International Maize and Wheat Improvement Center (CIMMYT), Mexico City); Gray, L. (Illinois State Univ., Urbana (USA)); Rayburn, A.L. (Illinois State Univ., Urbana (USA). Dept. of Agronomy)
Journal: Journal of Genetics and Breeding, Mar 1994, v. 48(1) p. 1-6
Notes: 12 ref. ISSN: 0394-9257
Language: English Summary Language: English
Place of Publication: Italy
Document Type: Journal Article, Summary
Journal Announcement: 2102 Record input by Italy
Abstract in English, Italiano
Randomly amplified polymorphic DNA (RAPD) markers were developed using the **polymerase chain** reaction (**PCR**) for the amphiploid of Triticum **aestivum** L. cv. Chinese Spring and Thinopyrum bessarabicum (Savul. and Rayss) Love. Polymorphisms observed with seven arbitrary oligonucleotide decamer **primers** are reported. There was no polymorphism among different DNA extracts from different individual seedlings of Chinese Spring. The amplification patterns generated with **primers** for the two plant species were repeatable. The marker bands specific to Th. bessarabicum may be helpful in tracking its chromatin in

the **wheat** background when chromosome additions, substitutions, translocations or subtile chromosomal interchanges are produced.

[I marcatori di DNA polimorfico amplificato randomizzato (RAPD) sono stati sviluppati per mezzo della reazione a catena polimerasica (**PCR**) per l'anfiploide di Triticum **aestivum** L. cv. Chinese Spring e Thinopyrum bessarabicum (Savul. e Rayss) Love. Vengono riferiti i polimorfismi osservati con sette iniettori decameri arbitrari di oligonucleotidi. Non si e' verificato polimorfismo tra estratti diversi di DNA di diverse piantine di Chinese spring. I modelli di amplificazione generati con gli iniettori per le due specie di piante erano ripetibili. Le bande di marcatori specifiche del Th. bessarabicum possono essere utili nel tracciare la sua cromatina nel grano quando si producono aggiunte di cromosomi, sostituzioni, trasferimenti o scambi cromosomici sottili].

? t s10/7/all

10/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09487694 BIOSIS NO.: 199497496064
Characterization of **minisatellites** in Arabidopsis thaliana with sequence similarity to the human **minisatellite** core sequence.

AUTHOR: Tourmente S(a); Deragon J M; Lafleuriel J; Tutois S; Pelissier T; Cuvillier C; Espagnol M C; Picard G
AUTHOR ADDRESS: (a)GDR 977 Biomove CNRS, Univ. Blaise Pascal, 24 Avenue des Landais, 63177 Aubiere Cedex, France

JOURNAL: Nucleic Acids Research 22 (16):p3317-3321 1994
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A strategy based on random PCR amplification was used to isolate new repetitive elements of Arabidopsis thaliana. One of the random PCR product analyzed by this approach contained a tandem repetitive **minisatellite** sequence composed of 33 bp repeated units. The genomic locus corresponding to this PCR product was isolated by screening a lambda genomic library. New related loci were also isolated from the genomic library by screening with a 14 mer oligonucleotide representing a region conserved among the different repeated units. Alignment of the consensus sequence for each **minisatellite** locus allowed the definition of an Arabidopsis thaliana core sequence that shows strong sequence similarities with the human core sequence and with the generalized recombination signal Chi of Escherichia coli. The **minisatellites** were tested for their ability to detect **polymorphism**, and their chromosomal position was established.

10/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09350704 BIOSIS NO.: 199497359074
Extraordinarily **polymorphic microsatellite** DNA in barley: Species diversity, chromosomal locations, and population dynamics.

AUTHOR: Maroof M A Saghai(a); Biyashev R M; Yang G P; Zhang Q; Allard R W
AUTHOR ADDRESS: (a)Dep. Crop Soil Environmental Sci., Virginia Polytechnic Inst. State Univ., Blacksburg, VA 24061, USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (12):p5466-5470 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This study was undertaken to assess the extent of genetic variation in barley **simple** sequence **repeats** (SSRs) and to

study the evolutionary dynamics of SSR alleles. SSR **polymorphisms** were resolved by the polymerase chain reaction with four pairs of primers. In total, 71 variants were observed in a sample of 207 accessions of wild and cultivated barley. Analyses of **wheat**-barley addition lines and barley doubled haploids identified these variants (alleles) with four loci, each located on a different chromosome. The numbers of alleles detected at a locus corresponded to the number of nucleotide repeats in the **microsatellite** sequences. The numbers of alleles at two loci were 28 and 37; to our knowledge these are the largest numbers of alleles for single Mendelian loci reported in **plants**. Three alleles were resolved by each of the other two loci. Allelic diversity was greater in wild than in cultivated barley and surveys of two generations (F-8 and F-53) of Composite Cross II, an experimental population of cultivated barley, showed that few of the alleles present in the 28 parents survived into generation F-53, whereas some infrequent alleles reached high frequencies. Such changes in frequency indicate that the chromosomal segments marked by the SSR alleles are under the influence of natural selection. The SSR variants allow specific DNA sequences to be followed through generations. Thus, the great resolving power of SSR assays may provide clues regarding the precise targets of natural and man-directed selection.

10/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09230396 BIOSIS NO.: 199497238766
Chromosomal localization and **polymorphisms** of ribosomal DNA in oat (Avena spp.).

AUTHOR: Jellen E N; Phillips R L(a); Rines H W
AUTHOR ADDRESS: (a)Dep. Agronomy and Plant Genetics, Plant Molecular Genetics Inst., Univ. Minn., St. Paul, MN 5510, USA

JOURNAL: Genome 37 (1):p23-32 1994
ISSN: 0831-2796
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; French

ABSTRACT: The 17S/5.8S/26S ribosomal DNA (rDNA) sequences were mapped to the three **satellited** (SAT) chromosomes in the common hexaploid cultivated oat Avena sativa (2n = 6x = 42, AACCDD genomes). In situ hybridization and Southern hybridization of maize and (or) **wheat** rDNA probes to DNA from nullisomics derived from the cultivar 'Sun II' allowed the placement of rDNA sequences to the physical chromosomes. A restriction map was produced for the rDNA sequences of 'Sun II' using a maize probe from the transcribed region of the 17S/26S rDNA repeat. The set of rDNA repeats on SAT 2 of 'Sun II' possesses a 10.5-kb EcoRI fragment not found in the rDNA repeats of SAT I and SAT 8. This 10.5-kb fragment results from the absence of an EcoRI site in the intergenic spacer (IGS) of SAT 2 repeats. Extensive **polymorphisms** were demonstrated for three hexaploid Avena species, namely, the Mediterranean-type cultivated oat A. byzantina and the wild species A. sterilis and A. fatua. However, geographically diverse A. sativa cultivars displayed little rDNA variation. In contrast with all of the A. sativa cultivars examined, the A. sterilis accessions generally lacked the 10.5-kb EcoRI fragment. The results support the hypothesis that A. sativa accessions descend from a limited ancestral cultivated population. The rDNA **polymorphisms** are attributed to differences in lengths and restriction sites of the IGS.

10/7/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

09086990 BIOSIS NO.: 199497095360
Restriction fragment length **polymorphism** analysis of variation in Fusarium species causing ear blight of cereals.

AUTHOR: Nicholson P(a); Jenkinson P; Rezanoor H N(a); Parry D W
AUTHOR ADDRESS: (a)Cambridge Lab., Inst. Plant Science Res., John Innes Centre, Colney Lane, Norwich NR4 7UJ, UK

JOURNAL: Plant Pathology (Oxford) 42 (6):p905-914 1993
ISSN: 0032-0862
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genetic variation in Fusarium species on **wheat** was investigated using restriction fragment length **polymorphism** (RFLP) analysis. Single-spore lines (76) of Fusarium were recovered from 24 ears of **wheat** in a field plot exhibiting severe symptoms of Fusarium ear blight and identified using classical taxonomic criteria. Four Fusarium species were present, of which F. avenaceum and F. culmorum were predominant with F. lateritium and F. poae present in two ears and one ear, respectively. RFLP analysis using rDNA (pTA71) or total genomic DNA from an F. culmorum isolate clearly distinguished the four species. Genetic fingerprints of the isolates generated using DNA of bacteriophage M13 (which contains a mini-**satellite** repeat sequence) revealed considerable variation within three of the four species (except F. poae). Generally, only a single clone was recovered from each ear and in all but one case only a single species was obtained from each spikelet. However, in several instances it appeared that more than one clone of a species was present within a single spikelet.

10/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08912024 BIOSIS NO.: 199396063525
Genetic and physical mapping of barley telomeres.

AUTHOR: Roder Marion S(a); Lapitan Nora L V; Sorrells Mark E; Tanksley Steven D
AUTHOR ADDRESS: (a)Dep. Plant Breeding and Biometry, Cornell Univ., 252 Emerson Hall, Ithaca, NY 14853, USA

JOURNAL: Molecular & General Genetics 238 (1-2):p294-303 1993
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Barley (Hordeum vulgare L.) telomeres were investigated by means of pulsed field gel electrophoresis (PFGE) and in situ hybridization. In situ hybridization showed that a tandemly repeated **satellite** sequence has a subtelomeric location, and is present at thirteen of the fourteen chromosome ends. PFGE revealed that this **satellite** sequence is physically close to the telomeric repeat. Pulsed field gel electrophoresis was then used for segregation analysis and linkage mapping of several telomeric and **satellite** loci in a segregating doubled-haploid population. The telomeric repeat displayed a hypervariable segregation pattern with new alleles occurring in the progeny. Eight **satellite** and telomeric sites were mapped on an restriction fragment length **polymorphism** (RFLP)-map of barley, defining the ends of chromosome arms 1L, 2S, 3L, 4S, 4L, 5S and 6. One

satellite locus mapped to an interstitial site on the long arm of chromosome 3. The physical location of this locus was confirmed by in situ hybridization to **wheat**/barley addition line 3.

10/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08204861 BIOSIS NO.: 000094017134
5S RIBOSOMAL GENE CLUSTERS IN **WHEAT** PULSED FIELD GEL ELECTROPHORESIS REVEALS A HIGH DEGREE OF **POLYMORPHISM**

AUTHOR: RODER M S; SORRELLS M E; TANKSLEY S D
AUTHOR ADDRESS: DEP. PLANT BREEDING BIOMETRY, CORNELL UNIV., 252 EMERSON HALL, ITHACA, N.Y. 14853.

JOURNAL: MOL GEN GENET 232 (2). 1992. 215-220.
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The long-range structure of 5S rRNA gene clusters has been investigated in **wheat** (**Triticum** aestivum L.) by means of pulsed field gel electrophoresis. Using aneuploid stocks, 5S rRNA gene clusters were assigned to sites on chromosomes 1B, 1D, 5B and 5D. Cluster sizes were evaluated and the copy number of 5S DNA repeats was estimated at 4700-5200 copies for the short repeating unit (410 bp) and about 3100 copies for the long repeat (500 bp) per haploid genome. A comparison of **wheat** cultivars revealed extremely high levels of **polymorphism** in the 5S rRNA gene clusters. With one restriction enzyme digest all varieties tested gave unique banding patterns and, on a per fragment basis, 21-fold more **polymorphism** was detected among cultivars for 5S DNA compared to standard restriction fragment length **polymorphisms** (RFLPs) detected with single copy clones. Experiments with aneuploid stocks suggest that the 5S rRNA gene clusters at several chromosomal sites contribute to this **polymorphism**. A number of previous reports have shown that **wheat** cultivars are not easily distinguished by isozymes or RFLPs. The high level of variation detected in 5S rRNA gene clusters therefore offers the possibility of a sensitive fingerprinting method for **wheat**. 5S DNA and other macro-**satellite** sequences may also serve as hypervariable Medelian markers for genetic and breeding experiments in **wheat**.

10/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07928576 BIOSIS NO.: 000093016974
REPETITIVE DNA SEQUENCES FROM POLYPLOID ELYMUS-TRACHYCAULUS AND THE DIPLOID PROGENITOR SPECIES DETECTION AND GENOMIC AFFINITY OF ELYMUS CHROMATIN ADDED TO **WHEAT**

AUTHOR: TSUJIMOTO H; GILL B S
AUTHOR ADDRESS: DEP. PLANT PATHOL., KANSAS STATE UNIV., MANHATTAN, KANSAS 66506-5502, USA.

JOURNAL: GENOME 34 (5). 1991. 782-789.
FULL JOURNAL NAME: Genome
CODEN: GENOE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A set of four repetitive DNA clones, pEt1, pEt2, pCb1, and pCb3,

were isolated from SH-genome polyploid Elymus trachycaulus and H-genome diploid Critesion bogdanii. The clone Et1 represents a tandemly arranged telomeric sequence. Et2 represents **tandem repeats** interspersed along the entire length of individual chromosomes. The Cb1 sequence was more evenly dispersed. The Et1 clone shared homology with a 350 base pair family of rye sequences. The Cb3 sequence was evenly distributed in S- and H-genome species. All the repetitive DNA sequences were excellent markers for the specific detection and genomic affinity of Elymus chromatin added to **wheat**. All clones showed intragenomic variation in copy number and chromosomal location. Based on the analysis of this variation, we conclude that E. trachycaulus most probably originated from putative diploid H- and S-genome species resembling Critesion californicum and Pseudoroegneria spicata, respectively.

10/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07608014 BIOSIS NO.: 000091125898
GENETIC LINKAGE BETWEEN C-BANDS AND STORAGE PROTEIN GENES IN CHROMOSOME 1B OF TETRAPLOID **WHEAT**

AUTHOR: CURTIS C A; LUKASZEWSKI A J
AUTHOR ADDRESS: DEP. BOTANY PLANT SCIENCES, UNIV. CALIF., RIVERSIDE, CALIF. 92521, USA.

JOURNAL: THEOR APPL GENET 81 (2). 1991. 245-252.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Genetic mapping of **polymorphic** C-bands allows direct comparisons between genetic and physical maps. Eleven C-bands and two seed storage protein genes on chromosome 1B, **polymorphic** between Langdon durum and four accessions of **Triticum** dicoccoides, were used to study the distribution of recombination along the entire length of the chromosome. Recombination in the short arm was almost completely restricted to the **satellite**, two-thirds of the arm's length from the centromere; the Gli-B1 gene was found to be tightly linked to the telomeric C-band. In the long arm, the distal 51.4% of the arm accounted for 88% of recombination; the proximal half of the arm accounted for the remaining 12%. While the amount of crossing-over differed significantly between the four T. dicoccoides 1B chromosomes, there were no significant differences in the relative distributions of crossing-over along the chromosome. Consequently, the genetic maps obtained from the four individual T. dicoccoides chromosomes were combined to yield a consensus map of 14 markers (including the centromere) for the chromosome.

10/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07356006 BIOSIS NO.: 000090134914
CHARACTERIZATION OF RELIC DNA FROM BARLEY GENOME

AUTHOR: BELOSTOTSKY D A; ANANIEV E V
AUTHOR ADDRESS: DIV. CELL BIOL. ENGL., UKRAINIAN SSR ACAD. SCI., LEBEDEV STR. 1, KIEV 252650, USSR.

JOURNAL: THEOR APPL GENET 80 (3). 1990. 374-380.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: High-molecular-weight "relic" DNA fraction can be electrophoretically separated form the bulk of barley DNA digested with different restriction enzymes. We have cloned and analyzed a population of relic DNA fragments. The majority of AluI-relic DNA clones contained barley simple sequence **satellite** DNA and other families of repetitive DNA. One of these families, designated HvRT, has been analysed in detail. This family is composed of tandemly arranged 118-bp monomers and is present in 7 .times. 105 copies in the barley genome. Clones representing the HvRT family were sequenced. HvRT repeats were found to contain high levels of methylated cytosine. The HvRT family was found in the genomes of H. vulgare, H. leporinum, H. murinum, H. jubatum, but not in H. marinum, H. geniculatum, and **wheat**. Different barley species and cultivars show restriction fragment length **polymorphism** with the HvRT probe. Chromosome-specific subfamilies of HvRT were found to be present on different barley chromosomes, proving the possibility of using the HvRT probe as a chromosome-specific marker. HvRT fragments up to 810 kbp in length were resolved by pulsed field gel electrophoresis.

10/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07270958 BIOSIS NO.: 000090050837
STRUCTURAL ANALYSIS OF THE SHORT LENGTH RIBOSOMAL DNA VARIANT FROM PISUM-SATIVUM L. CULTIVAR ALASKA

AUTHOR: PILLER K J; BAERSON S R; POLANS N O; KAUFMAN L S
AUTHOR ADDRESS: UNIVERSITY ILLINOIS CHICAGO, PO BOX 4348, M/C 067, CHICAGO, IL 60680, USA.

JOURNAL: NUCLEIC ACIDS RES 18 (11). 1990. 3135-3146.
FULL JOURNAL NAME: Nucleic Acids Research
CODEN: NARHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The genomic clone, RRNpss1, representing the short ribosomal DNA length variant in Pisum sativum L. cv. Alaska, has been isolated and the 2859 bp intergenic spacer, along with the 25S rRNA 3' border and 18S rRNA 5' border, has been sequenced. The intergenic spacer contains nine **tandem repeats**, approximately 180 bp in length, which show greater than 80% sequence homology to each other. The RNA polymerase I transcription start site and a processing site, located 776 bp and 536 bp upsteam of the 5' end of 18S rRNA, respectively, have been determined using S1 analysis. The region surrounding the +1 site shows strong homology between the positions -6 to +10 to the rDNA sites of initiation in radish, maize, and **wheat**. The sequence CATGCAAA is located 19 bp upstream of the site of initiation, and appears once within each subrepeat and twice more between the end of the subrepeat array and the site of initiation. A previously characterized HpaII site which shows developmental regulation of methylation is located 31 bp downstream of the site of initiation. Using RFLP linkage analysis, the short rDNA length variant of cv. Alaska is assigned to Chromosome 4 where it is genetically independent of the long rDNA length variant which is putatively assigned to Chromosome 7.

10/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06764383 BIOSIS NO.: 000088073816
AN UNUSUAL **WHEAT** INSERTION SEQUENCE WIS1 LIES UPSTREAM OF AN ALPHA

AMYLASE GENE IN HEXAPLOID **WHEAT** AND CARRIES A **MINISATELLITE** ARRAY

AUTHOR: MARTIENSSEN R A; BAULCOMBE D C
AUTHOR ADDRESS: SAINSBURY LAB., JOHN INNES INST., COLNEY LANE, NORWICH NR4 7UH, UK.

JOURNAL: MOL GEN GENET 217 (2-3). 1989. 401-410.
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Comparison of the 5' flanking regions of three .alpha.-amylase genes from chromosome 6B of hexaploid **wheat** by heteroduplex and sequence analysis revealed the presence of a 1.6kb stem-loop insertion sequence (WIS1) in one of them. **Polymorphism** among hexaploid **wheat** varieties suggests the relatively recent insertion/excision of this sequence from its present position. The complete sequence of the stem-loop insertion shows that it has many of the features found in transposable elements, including target site duplication and terminal inverted repeats. One unusual feature is a **tandem** array of direct **repeats** comprising a **wheat "minisatellite"** sequence. Both the insertion sequence and the **minisatellite** are found at multiple locations in the **wheat** genome, but the functional significance of their association in WIS1 is unknown. The **minisatellite** arrays share a common core structure, and long arrays are **polymorphic** between different hexaploid varieties.

10/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06628486 BIOSIS NO.: 000087070648
ORGANIZATION AND THE PRIMARY NUCLEOTIDE SEQUENCE OF THE 5S RIBOSOMAL RNA GENES IN BARLEY HORDEUM-VULGARE

AUTHOR: KHVYRLEVA TS D; GAZUMYAN A K; ANAN'EV E V
AUTHOR ADDRESS: N.I. VAVILOV INST. GEN. GENET., ACAD. SCI. USSR, MOSCOW, USSR.

JOURNAL: GENETIKA 24 (0). 1988. 1830-1840.
FULL JOURNAL NAME: Genetika
CODEN: GNKAA
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: A BamHI DNA fragment of 301 bp corresponding to the main repeating unit of 5S rRNA was isolated from barley genomic DNA. The primary nucleotide sequence of this fragment was determined and a high level of homology was found between coding sequences of 5S rRNA genes of barley, **wheat** and rye. At the same time, spacer's nucleotide sequences of different species of cereals were changed dramatically. At least two types of 5S rRNA **tandem repeats** of 301 and 450 bp were found in barley genome. **Polymorphism** for restriction fragment length in 5S rRNA repeats allowed to discriminate between all barley varieties used in this work.

10/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06098815 BIOSIS NO.: 000085061964
AMINO-TERMINAL SEQUENCES OF OAT AVENINS COMPARED TO OTHER CEREAL PROLAMINS

AUTHOR: PERNOLLET J-C; HUET J-C; GALLE A-M; SALLANTIN M
AUTHOR ADDRESS: LAB. D'ETUDES DES PROTEINES, CENT. INRA, ROUTE DE ST.-CYR, 78000 VERSAILLES, FRANCE.

JOURNAL: BIOCHIMIE (PARIS) 69 (6-7). 1987. 683-690.
FULL JOURNAL NAME: BIOCHIMIE (Paris)
CODEN: BICMB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Like the alcohol-soluble seed storage proteins (also called prolamins) of other cereals, avenins, the oat prolamins, are a series of **polymorphic** molecules belonging to a multigenic family stored within the protein bodies of the starchy endosperm. Nevertheless, they exhibit some pecularities: among the seed storage proteins, their proportion is low compared to prolamins from other cereal species; their net charge is higher; the amount of Gln + Pro only reaches 49 mol%; they are less **polymorphic**. We have isolated and purified several avenins and sequenced their N-terminal end. The microheterogeneity and the pecularity of avenins are revealed by the comparison of the N-terminal sequences. Like other prolamins, they exhibit **tandem repeats**; these repetitive peptides are slightly different from those of other prolamins of the Festucoideae, and the repetition begins earlier in the sequence. As for prolamins from other species their predicted secondary structure reveals successive .beta.-turns which might be arranged in a pseudo-helix structure.

10/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

04764540 BIOSIS NO.: 000080067667
EVOLUTION AND HETEROGENEITY OF THE ALPHA-BETA-TYPE AND GAMMA-TYPE GLIADIN DNA SEQUENCES

AUTHOR: OKITA T W; CHEESBROUGH V; REEVES C D
AUTHOR ADDRESS: INST. BIOL. CHEM., WASH. STATE UNIV., PULLMAN, WASH. 99164-6340.

JOURNAL: J BIOL CHEM 260 (13). 1985. 8203-8213.
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Near full length c[complementary]DNA clones for both .alpha.-/.beta.- and .gamma.-type gliadins were isolated and studied for sequence diversity. Based on restriction site **polymorphism** and cross-hybridization studies, .alpha.-/.beta.- and .gamma.-type clones could be divided into 5 and 3 homology classes, respectively. Clones representing each of the different classes were sequenced and compared. Sequence divergence between the classes was due to single-base substitutions and to duplications or deletions within or near direct repeats. Through numerous duplications and subsequent divergence, the gliadin multigene family encodes a **polymorphic** set of polypeptides differing in both isoelectric point and molecular size. Southern blot analysis of **wheat** DNA suggested that the number of genes encoding the .alpha.-/.beta.-type gliadins was extremely large (> 100 copies/haploid genome). Inasmuch as hybridization patterns were the same using DNA isolated from seeds or leaves, amplification or rearrangement of DNA does not occur during development. The complete coding sequence of a .gamma.-gliadin was similar to that observed for the .alpha.-/.beta.-gliadins, but with several notable differences. Comparison of .gamma.-type gliadin cDNA sequences showed that, unlike the

conserved dodecamer repeat common to all the .alpha.-/.beta.-gliadins, the **tandem repeat** unit differed among .gamma.-gliadin clones.

10/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

04682144 BIOSIS NO.: 000079095273
INTRACHROMOSOMAL MAPPING OF THE NUCLEOLAR ORGANIZER REGION RELATIVE TO 3 MARKER LOCI ON CHROMOSOME 1B OF **WHEAT TRITICUM**-AESTIVUM

AUTHOR: SNAPE J W; FLAVELL R B; O'DELL M; HUGHES W G; PAYNE P I
AUTHOR ADDRESS: PLANT BREEDING INSTITUTE, TRUMPINGTON, CAMBRIDGE CB2 2LQ, ENGLAND.

JOURNAL: THEOR APPL GENET 69 (3). 1985. 263-270.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Restriction enzyme digestion of the rRNA genes of the nucleolar organizers of wheats revealed fragment length **polymorphisms** for the nucleolar oragnizer on chromosome 1B and the nucleolar organizer on 6B. Variation between genotypes for these regions was also demonstrated. This variation was exploited to determine the recombination frequency between the physically defined nucleolar organizer on 1B (designated Nor1) and other markers: 2 loci, Glu-B1 and Gli-B1 which code for endosperm storage proteins and Rf3, a locus restoring fertility to male sterility conditioned by T. timopheevi cytoplasm. Gli-B1 and Rf3 were located on the short-arm **satellite**, but recombine with the nucleolar organizer giving a gene order of Nor1-Rf3-Gli-B1. Glu-B1 is located on the long arm of 1B, but shows relatively little recombination with Nor1, which is, in physical distance, distal on the short arm. This illustrates the discrepancy between map distance and physical distance on **wheat** chromosomes due to the distal localization of chiasmata. The recombination between Nor1 and Rf3 indicates that, contrary to previous suggestions, fertility restoration is not a property of the nucleolar organizer but of a separate locus.

10/7/16 (Item 1 from file: 35)
DIALOG(R)File 35:Dissertation Abstracts Online

01409671 ORDER NO: AADAA-I9513701
GENETIC MAPS OF RYE CHROMOSOMES 1R, 6R, AND 7R INTEGRATING RFLP AND CYTOGENIC LOCI

Author: WANOUS, MICHAEL K.
Degree: PH.D.
Year: 1994
Corporate Source/Institution: UNIVERSITY OF MISSOURI - COLUMBIA (0133)
Supervisor: J. PERRY GUSTAFSON
Source: VOLUME 55/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 5185. 67 PAGES

Genetic maps of rye chromosomes 1R, 6R, and 7R were placed within the context of the physical architecture of the chromosomes. This allowed for an analysis of the relationship between the genetic and cytological maps and put ends on the genetic maps.

An immortalized F$\sb2$ mapping population was created from a cross between UC-90 and E-line rye, which are **polymorphic** for eight C-band loci. This mapping project involved the screening of 385 clones and C-banding of 111 F$\sb2$ **plants**. The following levels of **polymorphism** were found for the various classes of clones: rye gDNA

46%; **wheat** cDNA 65%; **wheat** gDNA 60%; barley cDNA 48%; and oat cDNA 30%. The level of **polymorphism** detected with restriction enzymes was as follows: DraI 30%; EcoRV 26%; EcoRI 23%; and HindIII 19%.

A genetic map of rye chromosome 1R covering 247 cM from terminal C-band to terminal C-band was constructed utilizing 27 RFLP and four C-band markers. Genetic mapping of C-bands and the centromere and in situ hybridization of three genetically mapped clones, allowed the genetic and cytological maps to be integrated. Eight contact points between the genetic and cytological maps revealed variation in the recombination distance to cytological distance ratio ranging between 0.25 and 1.95, a 7.8-fold difference. Recombination was found to be highest in the **satellite** of 1RS and least in the most distal region of 1RL.

RFLP genetic maps of rye chromosomes 6R and 7R were generated, with 6R including both terminal C-bands, and 7R including the 7RS terminal C-band. The 6R map spans 230 cM and includes nine loci The 7R map covers 221 cM and includes 20 loci. Segregation distortion was detected for several chromosomal regions. For common intervals between the present maps and a previous rye RFLP map (Devos et al. 1993), genetic distances (cM) were greater for the present map by a factor of 2.2.

10/7/17 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

04309520 EMBASE No: 1990192076
Structural analysis of the short length ribosomal DNA variant from Pisum sativum L. cv. Alaska
Piller K.J.; Baerson S.R.; Polans N.O.; Kaufman L.S.
Laboratory for Cell, Molecular and Developmental Biology, Department of Biological Sciences, University of Illinois at Chicago, Chicago, IL 60680 United States
Nucleic Acids Research (NUCLEIC ACIDS RES.) (United Kingdom) 1990, 18/11 (3135-3145)

CODEN: NARHA ISSN: 0305-1048
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The genomic clone, RRNpss1, representing the short ribosomal DNA length variant in Pisum sativum L. cv. Alaska, has been isolated and the 2859 bp intergenic spacer, along with the 25S rRNA 3' border and 18S rRNA 5' border, has been sequenced. The intergenic spacer contains nine **tandem repeats**, approximately 180 bp in length, which show greater than 80% sequence homology to each other. The RNA polymerase I transcription start site and a processing site, located 776 bp and 536 bp upstream of the 5' end of 18S rRNA, respectively, have been determined using S1 analysis. The region surrounding the +1 site shows strong homology between the positions -6 to +10 to the rDNA sites of initiation in radish, maize, and **wheat**. The sequence CATGCAAA is located 19 bp upstream of the site of initiation, and appears once within each subrepeat and twice more between the end of the subrepeat array and the site of initiation. A previously characterized HpaII site which shows developmental regulation of methylation is located 31 bp downstream of the site of initiation. Using RFLP linkage analysis, the short rDNA length variant of cv. Alaska is assigned to Chromosome 4 where it is genetically independent of the long rDNA length variant which is putatively assigned to Chromosome 7.

10/7/18 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07925528 94261606
Extraordinarily **polymorphic microsatellite** DNA in barley: species diversity, chromosomal locations, and population dynamics.

Saghai Maroof MA; Biyashev RM; Yang GP; Zhang Q; Allard RW
Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg 24061.
Proc Natl Acad Sci U S A (UNITED STATES) Jun 7 1994, 91 (12) p5466-70, ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: JOURNAL ARTICLE
This study was undertaken to assess the extent of genetic variation in barley **simple** sequence **repeats** (SSRs) and to study the evolutionary dynamics of SSR alleles. SSR **polymorphisms** were resolved by the polymerase chain reaction with four pairs of primers. In total, 71 variants were observed in a sample of 207 accessions of wild and cultivated barley. Analyses of **wheat**-barley addition lines and barley doubled haploids identified these variants (alleles) with four loci, each located on a different chromosome. The numbers of alleles detected at a locus corresponded to the number of nucleotide repeats in the **microsatellite** sequences. The numbers of alleles at two loci were 28 and 37; to our knowledge these are the largest numbers of alleles for single Mendelian loci reported in **plants**. Three alleles were resolved by each of the other two loci. Allelic diversity was greater in wild than in cultivated barley and surveys of two generations (F8 and F53) of Composite Cross II, an experimental population of cultivated barley, showed that few of the alleles present in the 28 parents survived into generation F53, whereas some infrequent alleles reached high frequencies. Such changes in frequency indicate that the chromosomal segments marked by the SSR alleles are under the influence of natural selection. The SSR variants allow specific DNA sequences to be followed through generations. Thus, the great resolving power of SSR assays may provide clues regarding the precise targets of natural and man-directed selection.

10/7/19 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05519410 89172009
[Organization and primary nucleotide sequence of 5S rRNA genes in barley Hordeum vulgare]
Organizatsiia i pervichnaia nukleotidnaia posledovatel'nost' genov 5S pRNK u iachmenia (Hordeum vulgare).
Khvyrleva TsD; Gazumian AK; Anan'ev EV
Genetika (USSR) Oct 1988, 24 (10) p1830-40, ISSN 0016-6758 Journal Code: FNN
Languages: RUSSIAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE English Abstract
A BamHI DNA fragment of 301 bp corresponding to the main repeating unit of 5S rRNA was isolated from barley genomic DNA. The primary nucleotide sequence of this fragment was determined and a high level of homology was found between coding sequences of 5S rRNA genes of barley, **wheat** and rye. At the same time, spacer's nucleotide sequences of different species of cereals were changed dramatically. At least two types of 5S rRNA **tandem repeats** of 301 and 450 bp were found in barley genome. **Polymorphism** for restriction fragment length in 5S rRNA repeats allowed to discriminate between all barley varieties used in this work.

10/7/20 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA

3339542 20368605 Holding Library: AGL
Pre-germination genotypic screening using PCR amplification of half-seeds
Chunwongse, J. Martin, G.B.; Tanksley, S.D.
Berlin, W. Ger. : Springer International.
Theoretical and applied genetics. July 1993. v. 86 (6) p. 694-698.
ISSN: 0040-5752 CODEN: THAGA6

DNAL CALL NO: 442.8 Z8
Language: English
Includes references
Place of Publication: Germany, West
Subfile: IND; OTHER FOREIGN;
Document Type: Article

A simple and rapid PCR-based method has been developed for determining the genotype of seeds before germination. Single half-seeds of **rice** (**Oryza** sativa L.) and **wheat** (**Triticum** aestivum L. em. Thell.) were preincubated, without grinding, in an aqueous extraction buffer. The resulting supernatants were then used in polymerase chain reaction (PCR) with oligonucleotide primers corresponding to **rice** single-copy sequences or a **wheat microsatellite** repeat. PCR products of identical size were amplified using either the half-seed extract or DNA isolated from leaf tissue. The remnant half-seeds can be maintained in ordered arrays using microtiter plates allowing the recovery of selected genotypes. Pre-germination genotypic screening of seed populations as described in this report should be useful for a variety of applications in **plant** breeding and genetics studies.

10/7/21 (Item 1 from file: 203)
DIALOG(R)File 203:AGRIS

01905377 AGRIS No: 95-111886
Characterization of a family of tandemly repeated DNA sequences in Triticeae

Vershinin, A. (Institute of Cytology and Genetics, Novosibirsk (Russian Federation)); Svitashev, S.; Gummesson, P.O.; Salomon, B.; Bothmer, R. von; Bryngelsson, T.

Journal: Theoretical and Applied Genetics, 1994, v. 89(2-3) p. 217-225
Notes: 3 ill., 1 graph, 2 tables; 45 ref. ISSN: 0040-5752
Language: English Summary Language: English
Place of Publication: Germany
Document Type: Journal Article, Summary
Journal Announcement: 2110 Record input by Germany

Abstract in English

The recombinant plasmid dpTa1 has an insert of relic **wheat** DNA that represents a family of tandemly organized DNA sequences with a monomeric length of approximately 340 bp. This insert was used to investigate the structural organization of this element in the genomes of 58 species within the tribe Triticeae and in 7 species representing other tribes of the Poaceae. The main characteristic of the genomic organization of dpTa1 is a classical ladder-type pattern which is typical for tandemly organized sequences. The dpTa1 sequence is present in all of the genomes of the Triticeae species examined and in one species from a closely related tribe (*Bromus inermis*, Bromeae). DNA from *Hordelymus europaeus* (Triticeae) did not hybridize under the standard conditions used in this study. Prolonged exposure was necessary to obtain a weak signal. The data suggest that the dpTa1 family is quite old in evolutionary terms, probably more ancient than the tribe Triticeae. The dpTa1 sequence is more abundant in the D-genome of **wheat** than in other genomes in Triticeae. DNA from several species also have bands in addition to the **tandem repeats** . The dpTa1 sequence contains short direct and inverted subrepeats and is homologous to a tandemly repeated DNA sequence from Hordeum chilense.

? t s12/7/all

12/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10178075 BIOSIS NO.: 199698632993
Detection of genetic diversity in closely related bread wheat using **microsatellite** markers.

AUTHOR: **Plaschke J**(a); **Ganal M W**; Roeder M S
AUTHOR ADDRESS: (a)Inst. Pflanzengenetik Kulturpflanzenforschung, Correnstr. 3, 06466 Gatersleben, Germany

JOURNAL: Theoretical and Applied Genetics 91 (6-7):p1001-1007 1995
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Wheat **microsatellites** (WMS) were used to estimate the extent of genetic diversity among 40 wheat cultivars and lines, including mainly European elite material. The 23 WMS used were located on 15 different chromosomes, and revealed a total of 142 alleles. The number of alleles ranged from 3 to 16, with an average of 6.2 alleles per WMS. The average dinucleotide repeat number ranged from 13 to 41. The correlation coefficient between the number of alleles and the average number of repeats was only slight (r-s = 0.55). Based on percentage difference a dendrogram is presented, calculated by the WMS-derived data. All but two of the wheat cultivars and lines could be distinguished. Some of the resulting groups are strongly related to the pedigrees of the appropriate cultivars. Values for co-ancestry (f) of 179 pairs of cultivars related by their pedigrees (f gtoreq 0.1) averaged 0.29. Genetic similarity (GS) based on WMS of the same pairs averaged 0.44. The rank correlation for these pairs was slight, with r-s = 0.55, but highly significant (P lt 0.001). The results suggest that a relatively small number of **microsatellites** can be used for the estimation of genetic diversity and cultivar identification in elite material of hexaploid bread wheat.

12/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09997324 BIOSIS NO.: 199598452242
Barley telomeres are associated with two different types of **satellite** DNA sequences.

AUTHOR: Brandes Andrea; **Roder Marion S**; **Ganal Martin W**(a
AUTHOR ADDRESS: (a)Inst. Pflanzengenetik Kulturpflanzenforschung, Correnssstrasse 3, 06466 Gatersleben, Germany

JOURNAL: Chromosome Research 3 (5):p315-320 1995
ISSN: 0967-3849
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The genomic organization of two different types of **satellite** DNA sequences was analysed by means of fluorescence in situ hybridization (FISH) and pulsed-field gel electrophoresis (PFGE) in barley. **Satellite** HvT01 was detected at all chromosome ends except the long arms of chromosomes 2 and 7. The unrelated **satellite** pAS1 was found at all chromosome ends except the long arm of chromosome 7 and at two interstitial sites, both located on the long arm of chromosome 4 on the standard karyotype. Southern and in situ hybridizations further indicate that pAS1 also occurs Interspersed in the barley genome. For most chromosome ends, the linear order of HvT01 and pAS1 could not be determined by in situ hybridization except at the short arms of chromosomes 2 and 6, where HvT01 is more distal than pAS1. This is confirmed by PFGE analysis, HvT01 being frequently associated with the telomeric repeat but not pAS1. Furthermore, we found that HvT01 occurred in clusters up to 1000 kb in size, whereas the pAS1 cluster had a maximum size of 500 kb. Sequence comparison revealed that both satellites are completely unrelated and differ considerably in their G + C contents.

12/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09724887 BIOSIS NO.: 199598179805
Abundance, variability and chromosomal location of **microsatellites** in wheat.

AUTHOR: Roeder Marion(a); **Plaschke Jeans**; Koenig Susanne U; Boerner Andreas; Sorrells Mark E; Tanksley Steven D; **Ganal Martin W**
AUTHOR ADDRESS: (a)Inst. Pflanzengenet. Kulturpflanzenforschung, Correnssstrasse 3, 06466 Gatersleben, Germany

Q1+426.M6

JOURNAL: Molecular & General Genetics 246 (3):p327-333 1995
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The potential of **microsatellite** sequences as genetic markers in hexaploid wheat (Triticum aestivum) was investigated with respect to their abundance, variability, chromosomal location and usefulness in related species. By screening a lambda phage library, the total number of (GA)-n blocks was estimated to be 3.6 times 10-4 and the number of (GT)-n blocks to be 2.3 x 10-4 per haploid wheat genome. This results in an average distance of approximately 270 kb between these two **microsatellite** types combined. Based on sequence analysis data from 70 isolated **microsatellites**, it was found that wheat **microsatellites** are relatively long containing up to 40 dinucleotide repeats. Of the tested primer pairs, 36% resulted in fragments with a size corresponding to the expected length of the sequenced **microsatellite** clone. The variability of 15 **microsatellite** markers was investigated on 18 wheat accessions. Significantly, more variation was detected with the **microsatellite** markers than with RFLP markers with, on average, 4.6 different alleles per **microsatellite**. The 15 PCR-amplified **microsatellites** were further localized on chromosome arms using cytogenetic stocks of Chinese Spring. Finally, the primers for the 15 wheat **microsatellites** were used for PCR amplification with rye (Secale cereale) and barley accessions (Hordeum vulgare, H. spontaneum). Amplified fragments were observed for ten primer pairs with barley DNA and for nine primer pairs with rye DNA as template. A **microsatellite** was found by dot blot analysis in the PCR products of barley and rye DNA for only one primer pair.

12/7/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

08912024 BIOSIS NO.: 199396063525
Genetic and physical mapping of barley telomeres.

AUTHOR: **Roder Marion S**(a); Lapitan Nora L V; Sorrells Mark E; Tanksley Steven D
AUTHOR ADDRESS: (a)Dep. Plant Breeding and Biometry, Cornell Univ., 252 Emerson Hall, Ithaca, NY 14853, USA

JOURNAL: Molecular & General Genetics 238 (1-2):p294-303 1993
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Barley (Hordeum vulgare L.) telomeres were investigated by means of pulsed field gel electrophoresis (PFGE) and in situ hybridization. In situ hybridization showed that a tandemly repeated **satellite** sequence has a subtelomeric location, and is present at thirteen of the fourteen chromosome ends. PFGE revealed that this **satellite** sequence is physically close to the telomeric repeat. Pulsed field gel electrophoresis was then used for segregation analysis and linkage mapping of several telomeric and **satellite** loci in a segregating doubled-haploid population. The telomeric repeat displayed a hypervariable segregation pattern with new alleles occurring in the progeny. Eight **satellite** and telomeric sites were mapped on an restriction fragment length polymorphism (RFLP)-map of barley, defining the ends of chromosome arms 1L, 2S, 3L, 4S, 4L, 5S and 6. One **satellite** locus mapped to an interstitial site on the long arm of chromosome 3. The physical location of this locus was confirmed by in situ hybridization to wheat/barley addition line 3.

12/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08204861 BIOSIS NO.: 000094017134
5S RIBOSOMAL GENE CLUSTERS IN WHEAT PULSED FIELD GEL ELECTROPHORESIS REVEALS A HIGH DEGREE OF POLYMORPHISM

AUTHOR: **RODER M S**; SORRELLS M E; TANKSLEY S D
AUTHOR ADDRESS: DEP. PLANT BREEDING BIOMETRY, CORNELL UNIV., 252 EMERSON HALL, ITHACA, N.Y. 14853.

JOURNAL: MOL GEN GENET 232 (2). 1992. 215-220.
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The long-range structure of 5S rRNA gene clusters has been investigated in wheat (Triticum aestivum L.) by means of pulsed field gel electrophoresis. Using aneuploid stocks, 5S rRNA gene clusters were assigned to sites on chromosomes 1B, 1D, 5B and 5D. Cluster sizes were evaluated and the copy number of 5S DNA repeats was estimated at 4700-5200 copies for the short repeating unit (410 bp) and about 3100 copies for the long repeat (500 bp) pier haploid genome. A comparison of wheat cultivars revealed extremely high levels of polymorphism in the 5S rRNA gene clusters. With one restriction enzyme digest all varieties tested gave unique banding patterns and, on a per fragment basis, 21-fold more polymorphism was detected among cultivars for 5S DNA compared to standard restriction fragment length polymorphisms (RFLPs) detected with single copy clones. Experiments with aneuploid stocks suggest that the 5S

rRNA gene clusters at several chromosomal sites contribute to this polymorphism. A number of previous reports have shown that wheat cultivars are not easily distinguished by isozymes or RFLPs. The high level of variation detected in 5S rRNA gene clusters therefore offers the possibility of a sensitive fingerprinting method for wheat. 5S DNA and other macro-**satellite** sequences may also serve as hypervariable Medelian markers for genetic and breeding experiments in wheat.

12/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08089845 BIOSIS NO.: 000093099918
TELOMERIC ARRAYS DISPLAY HIGH LEVELS OF HERITABLE POLYMORPHISM AMONG CLOSELY RELATED PLANT VARIETIES

AUTHOR: BROUN P; **GANAL M W**; TANKSLEY S D
AUTHOR ADDRESS: DEP. PLANT BREEDING BIOMETRY, CORNELL UNIVERSITY, ITHACA, N.Y. 14853.

JOURNAL: PROC NATL ACAD SCI U S A 89 (4). 1992. 1354-1357.
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Tomato [Lycopersicon esculentum] telomeres are composed of a terminal 7-base-pair **tandem repeat** and a closely linked 162-base-pair subtelomeric repeat (TGRI). Together, these repeats account for 2% of the total chromosomal DNA. Pulsed-field gel electrophoresis has been used to examine the long-range physical structure of these arrays in closely related varieties, and we report here that there arrays are undergoing heritable changes at a frequency as great as 2% per generation. Moreover, comparisons with other known hypervariable probes (e.g., human **minisatellites** and M13 sequences) revealed that telomeric sites are more variable than any other known region of the plant genome and can be used to distinguish closely related plant varieties (tomato and melon) [Cucumis melo]) that are otherwise very similar at the DNA level. The fact that the polymorphisms are inherited in a mendelian fashion suggests applications in genetic mapping of telomeres and identification of varieties.

12/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07499142 BIOSIS NO.: 000091073011
MACROSTRUCTURE OF THE TOMATO TELOMERES

AUTHOR: **GANAL M W**; LAPITAN L V; TANKSLEY S D
AUTHOR ADDRESS: DEP. PLANT BREEDING BIOMETRY, CORNELL UNIV., 252 EMERSON HALL, ITHACA, NY 14853.

JOURNAL: PLANT CELL 3 (1). 1991. 87-94.
FULL JOURNAL NAME: Plant Cell
CODEN: PLCEE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The macrostructure of the tomato telomeres has been investigated by in situ hybridization, genomic sequencing, and pulsed-field gel electrophoresis. In situ hybridizations with a cloned telomeric sequence from Arabdiopsis thaliana indicated that the telomeric repeat of tomato

cross-hybridizes with that of Arabidopsis and is located at all telomeres. Bal31 digestion kinetics confirmed that the tomato telomeric repeat represents the outermost DNA sequence of each tomato chromosome. Genomic sequencing of enriched tomato telomeric sequences, using primers derived from the Arabidopsis sequence, revealed that the consensus sequence of the tomato telomeric repeat is TT(T/A)AGGG compared with the Arabidopsis consensus sequence of TTTAGGG. Furthermore, as shown by pulsed-field gel electrophoresis, the telomeric repeat of tomato is separated by not more than a few hundred kilobases from a previously described 162-base pair **satellite** DNA repeat of tomato (TGR I) at 20 of the 24 telomeres. Together, these sequences are found in the heterochromatic terminal knob observed in pachytene chromosomes. Therefore, these two repeats determine the structure of 20 of the 24 tomato chromosome ends over approximately 2% of the total chromosome length.

12/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07012526 BIOSIS NO.: 000089104410
SOMATIC CHROMOSOME KARYOTYPE OF TOMATO BASED ON IN SITU HYBRIDIZATION OF THE TGRI **SATELLITE** REPEAT

AUTHOR: LAPITAN N L V; **GANAL M W**; TANKSLEY S D
AUTHOR ADDRESS: DEP. PLANT BREEDING BIOMETRY, 416 BRADFIELD HALL, CORNELL UNIV., ITHACA, N.Y. 14853, USA.

JOURNAL: GENOME 32 (6). 1989. 992-998.
FULL JOURNAL NAME: Genome
CODEN: GENOE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A karyotype of tomato mitotic chromosomes was constructed based on in situ hybridization to a 162 bp telomeric DNA repeat, TGRI. Variation in the spatial and quantitative distribution of this repeat creates distinct patterns for most of the chromosomes, which along with other morphological characteristics (i.e., length and arm length ratio), allow the identification of each of the 12 mitotic chromosomes of tomato. The structure and physical size of the TGRI clusters were further investigated by means of pulsed-field gel electrophoresis. Approximately 30 hybridizing fragments were observed in the range of 25 to 1000 kb when high molecular weight DNA was digested with BglII and probed with TGRI. The total molecular weight of these fragments is approximately 14 million bp, which is close to the estimated total length of TGRI in the genome (12.5 million bp) basedon genomic reconstruction experiments. The results suggest that most of the TGRI clusters consist of single, uninterrupted blocks of **satellite** DNA. Assignment of somatic chromosomes, identified by TGRI hybridization to the previously established tomato linkage gorups, were accomplished via in situ hybridization to mitotic spreads of primary trisomic lines. Using this information, we estimate the somatic length and DNA content of each of the tomato chromosomes and chromosome arms.

12/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06268520 BIOSIS NO.: 000086102703
A MOLECULAR AND CYTOGENETIC SURVEY OF MAJOR REPEATED DNA SEQUENCES IN TOMATO LYCOPERSICON-ESCULENTUM

AUTHOR: **GANAL M W**; LAPITAN N L V; TANKSLEY S D

AUTHOR ADDRESS: DEP. PLANT BREEDING AND BIOMETRY, 416 BRADFIELD HALL, CORNELL UNIV., ITHACA, NY 14853, USA.

JOURNAL: MOL GEN GENET 213 (2-3). 1988. 262-268.
FULL JOURNAL NAME: Molecular & General Genetics
CODEN: MGGEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The major families of repeated DNA sequences in the genome of tomato (Lycopersicon esculentum) were isolated from a sheared DNA library. One thousand clones, representing one million base pairs, or 0.15% of the genome, were surveyed for repeated DNA sequences by hybridization to total nuclear DNA. Four major repeat classes were identified and characterized with respect to copy number, chromosomal localization by in situ hybridization, and evolution in the family Solanaceae. The most highly repeated sequence, with approximately 77,000 copies, consists of a 162 bp tandemly repeated **satellite** DNA. This repeat is clustered at or near the telomeres of most chromosomes and also at the centromeres and interstitial sites of a few chromosomes. Another family of tandemly repeated sequences consists of the genes coding for the 45 S ribosomal RNA. The 9.1 kb repeating unit in L. esculentum was estimated to be present in approximately 2300 copies. The single locus, previously mapped using restriction fragment length polymorphisms, was shown by in situ hybridization as a very intense signal at the end of chromosome 2. The third family of repeated sequences was interspersed throughout nearly all chromosomes with an average of 133 kb between elements. The total copy number in the genome is approximately 4200. The fourth class consists of another interspersed repeat showing clustering at or near the centromeres in several chromosomes. This repeat had a copy number of approximately 2100. Sequences homologous to the 45 S ribosomal DNA showed cross-hybridization to DNA from all solanaceous species examined including potato, Datura, Petunia, tobacco and pepper. In contrast, with the exception of one class of interspersed repeats which is present in potato, all other repetitive sequences appear to be limited to the crossing-range of tomato. These results, along with those from a companion paper (Zamir and Tanksley 1988), indicate that tomato possesses few highly repetitive DNA sequences and those that do exist are evolving at a rate higher than most other genomic sequences.

12/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06203559 BIOSIS NO.: 000086037741
SPECIES-SPECIFIC DNA SEQUENCES FOR IDENTIFICATION OF SOMATIC HYBRIDS BETWEEN LYCOPERSICON-ESCULENTUM AND SOLANUM-ACAULE

AUTHOR: SCHWEIZER G; **GANAL M**; NINNEMANN H; HEMLEBEN V
AUTHOR ADDRESS: DEP. GENETIK, INST. BIOLOGIE II, UNIV. TUEBINGEN, AUF DER MORGENSTELLE 28, D-7400 TUEBINGEN, W. GER.

JOURNAL: THEOR APPL GENET 75 (5). 1988. 679-684.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Species-specific highly repeated DNA sequences can be used to screen the progeny of protoplast fusions combining different species. Such probes are easy to clone and can be detected by fast methods, e.g., hybridization to total genomic DNA. Furthermore, due to their high copy number, hybridization signals are strong and represent more than one locus, unlike isozymes or resistance markers. After cloning and screening for species-specific DNA sequences we characterized the highly repeated

DNA sequences of the solanaceous species Solanum acaule and Lycopersicon esculentum var. "gilva". DNA sequencing and hybridization revealed a prominent, tandemly arranged **satellite** DNA repeat of 162 bp in Lycopersicon esculentum and a different **satellite** repeat of 183 bp, also tandemly organized, in Solanum acaule. Each repeat is absent in the respective other species. Therefore, we have used these DNA repeats as markers to distinguish regenerated interspecific somatic hybrids from the respective fusion partners. These hybrids were clearly identified by Southern hybridization and dot-blot assays to the respective 32P-labelled **satellite** DNA.

12/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06126933 BIOSIS NO.: 000085090085
INSERTION AND AMPLIFICATION OF A DNA SEQUENCE IN **SATELLITE** DNA OF CUCUMIS-SATIVUS L. CUCUMBER

AUTHOR: **GANAL M**; HEMLEBEN V
AUTHOR ADDRESS: LEHRSTUHL FUER GENETIK, INST. FUER BIOL. II, UNIV. TUEBINGEN, AUF DER MORGENSTELLE 28, D-7400 TUEBINGEN, FEDERAL REPUBLIC OF GERMANY.

JOURNAL: THEOR APPL GENET 75 (2). 1988. 357-361.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Another **satellite** DNA repeat (type IV) in the genome of Cucumis sativus (cucumber) was found and investigated with respect to DNA sequence, methylation, and evolution. This **satellite** shows a repeat length of 360 bp and a GC-content of 47%. The repeats of type IV are highly conserved among each other. Evidence for CG and CNG methylation is presented. By comparison to the previously described satellites (type I/II and type III) from cucumber, it is evident that this repeat is created by an insertion of a 180 bp DNA sequence similar to type I-III into antoher DNA sequence (or vice versa), and subsequent amplification forming a new **satellite** repeat. The different satellites of the type I/II, type III, and the 180 bp insert of type IV show a sequence homology of 60%-70%, indicating that the complex **satellite** DNA of cucumber is originated from a common progenitor by mutation, additional insertion, and amplification events. Copies of a sequence similar to a part of type IV are present in the genome of the related species Cucumis melo (melon).

12/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05591920 BIOSIS NO.: 000083065060
DIFFERENT AT-RICH **SATELLITE** DNAS IN CUCURBITA-PEPO AND CUCURBITA-MAXIMA

AUTHOR: **GANAL M**; HEMLEBEN V
AUTHOR ADDRESS: LEHRSTUHL GENETIK, INST. BIOL. II, UNIV. TUEBINGEN, D-7400 TUEBINGEN, FRG.

JOURNAL: THEOR APPL GENET 73 (1). 1986. 129-135.
FULL JOURNAL NAME: Theoretical and Applied Genetics
CODEN: THAGA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The At-rich highly repeated **satellite** DNA of Cucurbita pepo (zucchini) and Cucurbita maxima (pumpkin) were cloned and their DNA structure was investigated. DNA sequencing revealed that the repeat length of **satellite** DNA in Cucurbita pepo is 349-352 base pairs. The percentage of AT-base pairs is about 61%. This **satellite** is highly conserved in restriction enzyme pattern and DNA sequence; sequence heterogeneity is about 10%. In contrast, the **satellite** DNA of Cucurbita maxima has a repeat length of 168-169 base pairs. This **satellite** is also rich in AT-base pairs (64%), existing in at least three different variants as revealed by restriction enzyme analysis and DNA sequencing. The sequence heterogeneity between these variants is about 15%. The two **satellite** DNAs showed no cross-hybridization to each other and sequence homology is only limited. Nevertheless, we found in the C. pepo genome a high amount of sequences resembling the **satellite** of C. maxima. In contrast, the **satellite** repeat of C. pepo is found in the C. maxima DNA only in a few copies. These observations were discussed with respect to **satellite** DNA evolution and compared to the data received from monocotyledonous species.

12/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05172929 BIOSIS NO.: 000082013550
ORGANIZATION AND SEQUENCE ANALYSIS OF TWO RELATED **SATELLITE** DNA SPECIES IN CUCUMBER CUCUMIS-SATIVUS

AUTHOR: **GANAL M**; RIEDE I; HEMLEBEN V
AUTHOR ADDRESS: DEP. GENET., INST. BIOL. II, UNIV. TUEB, 7400 TUEBINGEN, W. GER.

JOURNAL: J MOL EVOL 23 (1). 1986. 23-30.
FULL JOURNAL NAME: Journal of Molecular Evolution
CODEN: JMEVA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The highly repeated **satellite** DNA of Cucumis sativus (cucumber) represents about 20-30% of the total nuclear DNA. We have characterized the main elements of the enriched **satellite** DNA by restriction enzyme analysis, cloning, DNA sequencing, and DNA hybridization. About 85% of the **satellite** DNA composed of three types. Type I has a repeat length of 182 bp and a GC content of 47%. Type II is distinguished by a single base pair from type I; therefore type II must be referred to as a variant of type I. Type III, however, has an overall homology of only 59% to types I and II. The repeat length is 177 bp and the GC content is 53% for type III repeats. The molar ratio is about 4:1:2.5 among types I-III, respectively. Higher-order sequence organization was analyzed by hybridization with cloned type I and type III elements. The data indicate that in the cucumber genome types I/II and III DNA are organized as two separated satellites. Type I-III repeats of Cucumis sativus are not homologous to the main **satellite** of the closely related melon species Cucumis melo. However, there are DNA sequences present in a low amount in cucumber **satellite** DNA with some degree of homology to the main 352-bp-repeats in Cucumis melo. We discuss a model for the evolution of **satellite** DNA in the Cucumis species: From a common progenitor the two species have amplified different sequences of **satellite** DNA during evolution. Restriction enzyme analysis of cucumber **satellite** DNA with differently methylation-sensitive enzymes (Hpa II and Msp I) reveals that C methylation at both position of the -CCGG-recognition site is possible and for the most part does occur; however, in some repeats of the type I/II only the inner cytosine is methylated.

12/7/14 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

05197175 EMBASE No: 1992337409
Genetic mapping of tandemly repeated telomeric DNA sequences in tomato (Lycopersicon esculentum)
Ganal M.W.; Broun P.; Tanksley S.D.
Dept. of Plant Breeding/Biometry, Cornell University,Ithaca, NY 14853 United States
Genomics (GENOMICS) (United States) 1992, 14/2 (444-448)

CODEN: GNMCE ISSN: 0888-7543
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

A telomere-associated tandemly repeated DNA sequence of tomato, TGR I, has been used to map telomeres on the tomato RFLP linkage map. Mapping was performed by monitoring the segregation of entire arrays of TGR I from a segregating F2 population using pulsed-field gel electrophoresis (PFGE). With this strategy, four telomeres have been mapped to the ends of the short arm of chromosomes 9 and 12 and the long arms of chromosomes 5 and 11, using a saturated RFLP map of tomato containing approximately 1000 RFLP markers. In all four cases, the TGR I locus maps to the end of the chromosome, and the distance between the most distal single-copy RFLP marker and the telomeric TGR I locus was between 1.6 and 9.6 cM. This indicates that the region close to the telomeres does not show an excessive rate of recombination compared to other regions of the genome and that the RFLP map of tomato is essentially complete and covers the entire genome for all practical purposes. Additionally, the mapping technique presented here should be generally applicable to the mapping of other tandemly repeated DNA sequences.

12/7/15 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08577221 95247023
Pulsed-field gel analysis of 5S and **satellite** DNA in barley.
Roder MS; Sorrells ME; Tanksley SD
Institute for Plant Genetics and Crop Plant Research, Gatersleben, Germany.
Genome (CANADA) Feb 1995, 38 (1) p153-7, ISSN 0831-2796
Journal Code: FNP
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Pulsed-field gel electrophoresis was used to study the variability of clustered tandemly repeated sequences in barley. Twelve spring barley cultivars were investigated with a heterologous 5S DNA probe and the 118 base pair barley **satellite** DNA probe HVT01. On a per fragment basis, the 5S probe was 5 times and the barley **satellite** probe 6.7 times more variable than single- or low-copy RFLP markers, demonstrating their usefulness for cultivar distinction.

12/7/16 (Item 1 from file: 10)
DIALOG(R)File 10:AGRICOLA

3371557 20397236 Holding Library: AGL
Pulsed field gel electrophoresis, telomere mapping, and hypervariable markers for wheat
Roder, M.S. Sorrells, M.E.; Tanksley, S.D.
El Batan, Mexico : International Maize and Wheat Improvement Center,

[1992?]
Progress in genome mapping of wheat and related species : proceedings of the 3rd Public Workshop of the International Triticeae Mapping Initiative, 22-26 September 1992, CIMMYT, Mexico / p. 59-61.
ISBN: 9686127895
DNAL CALL NO: SB191.W5I579 1992
Language: English
Place of Publication: Mexico
Government Source: International
Subfile: IND; OTHER FOREIGN;
Document Type: Article

12/7/17 (Item 2 from file: 10)
DIALOG(R)File 10:AGRICOLA

3182072 92036333 Holding Library: AGL
Telomeric assays display high levels of heritable polymorphism among closely related plant varieties
Broun, P. **Ganal, M.W.**; Tanksley, S.D.
Cornell University, Ithaca, NY
Washington, D.C. : The Academy.
Proceedings of the National Academy of Sciences of the United States of America. Feb 15, 1992. v. 89 (4) p. 1354-1357.
ISSN: 0027-8424 CODEN: PNASA
DNAL CALL NO: 500 N21P
Language: English
Includes references.
Subfile: OTHER US (NOT EXP STN, EXT, USDA; SINCE 12/76);
Document Type: Article
Tomato telomeres are composed of a terminal 7-base-pair **tandem repeat** and a closely linked 162-base-pair subtelomeric repeat (TGRI). Together, these repeats account for 2% of the total chromosomal DNA. Pulsed-field gel electrophoresis has been used to examine the long-range physical structure of these arrays in closely related varieties, and we report here that these arrays are undergoing heritable changes at a frequency as great as 2% per generation. Moreover, comparisons with other known hypervariable probes (e.g., human **minisatellites** and M13 sequences) revealed that telomeric sites are more variable than any other known region of the plant genome and can be used to distinguish closely related plant varieties (tomato and melon) that are otherwise very similar at the DNA level. The fact that the polymorphisms are inherited in a mendelian fashion suggests applications in genetic mapping of telomeres and identification of varieties.